



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 143686

To: **Ruixiang Li**
Location: **rem/4d75/4c70**
Art Unit: **1646**
Wednesday, February 02, 2005

Case Serial Number: **09/881736**

From: **Beverly Shears**
Location: **Remsen Bldg.**
RM 1A54
Phone: **571-272-2528**

beverly.shears@uspto.gov

Search Notes

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From: Li, Ruixiang
 Sent: 78733 Sunday, January 30, 2005 2:41 PM
 To: STIC-Biotech/ChemLib
 Subject: Sequence search of Application No.09/881,736

Please do a standard search on:

SEQ ID NO: 2 against commercial amino acid databases.

99-632

Thank you very much!

Ruixiang Li
 GAU 1646
 REM 4D75
 Mail Box 4C70
 (571) 272-0875

MEJ

 STAFF USE ONLY

Searcher: _____
 Searcher Phone: 2-
 Date Searcher Picked up: _____
 Date Completed: _____
 Searcher Prep/Rev. Time: _____
 Online Time: _____

 Type of Search
 NA Sequence: # _____
 AA Sequence: # _____
 Structure: # _____
 Bibliographic: _____
 Litigation: _____
 Patent Family: _____
 Other: _____

 Vendors and cost where applicable
 STN: _____
 DIALOG: _____
 QUESTEL/ORBIT: _____
 LEXIS/NEXIS: _____
 SEQUENCE SYSTEM: _____
 WWW/Internet: _____
 Other(Specify): _____

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Date completed: Beverly e 2528
 Searcher: _____
 Terminal time: _____
 Elapsed time: _____
 CPU time: _____
 Total time: _____
 Number of Searches: _____
 Number of Databases: _____

Search Site
 _____ STIC
 _____ CM-1
 _____ Pre-S
 Type of Search
 _____ N.A. Sequence
 _____ A.A. Sequence
 _____ Structure
 _____ Bibliographic

Vendors
 _____ IG
 _____ STN
 _____ Dialog
 _____ APS
 _____ Geninfo
 _____ SDC
 _____ DARC/Questel
 _____ Other CRF

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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: February 1, 2005, 14:13:02 ; Search time 146 Seconds
(without alignments)
1563.938 Million cell updates/sec

Title: US-09-881-736A-2
Perfect score: 3243

Sequence: 1 MDTMLNVRNLFFQLVRRVE..... SKSATNLGRQGNFFASPMLK 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	3243	100.0	632 9 US-09-881-736-2	Sequence 2, Appli
2	3230	99.6	632 9 US-09-833-790-413	Sequence 413, Appli
3	2919	90.0	70 US-09-833-790-427	Sequence 427, Appli
4	2734	84.3	628 9 US-09-881-736-4	Sequence 4, Appli
5	1182	36.4	255 16 US-10-408-765A-1045	Sequence 1045, Appli
6	541.5	16.7	681 9 US-09-881-736-6	Sequence 6, Appli
7	334	10.3	2022 16 US-10-408-765A-598	Sequence 598, Appli
8	322	9.9	175 15 US-10-072-012-878	Sequence 878, Appli
9	322	9.9	175 15 US-10-072-012-879	Sequence 879, Appli
10	310	9.6	1261 15 US-10-072-012-733	Sequence 733, Appli
11	301	9.3	1261 14 US-10-177-980-2	Sequence 2, Appli
12	301	9.3	1261 16 US-10-648-593-192	Sequence 192, Appli
13	294.5	9.1	193 9 US-09-802-127-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-881-736-2
; Sequence 2, Application US/09881736
; Patent No. US20020076785A1
; GENERAL INFORMATION:
; APPLICANT: Glotzer, Michael
; APPLICANT: Jantsch-Plunger, Verena
; APPLICANT: Romano, Alper
; APPLICANT: Mishima, Masanori
; APPLICANT: Kaitna, Susanne
; TITLE OF INVENTION: CYK-4 polypeptides, DNA molecules encoding them and their use in
; TITLE OF INVENTION: screening methods
; FILE REFERENCE: 0652_226001/EKS/AES
; CURRENT APPLICATION NUMBER: US/09/881-736
; PRIOR APPLICATION NUMBER: EP 00 112 880.0
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: EP 01 110 554.1
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/241,231
; PRIOR APPLICATION NUMBER: To be determined
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-881-736-2
Query Match 100.0%; Score 3243; DB 9; Length 632;
Best Local Similarity 100.0%; Pred. No. 8.2e-258;
Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTMLNVRNLFFQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELGKYKDLIMK 60

RESULT 2
US-09-833-790-413
; Sequence 413, Application US/09833790
; Patent No. US-0020068288A1

GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Indrias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 413
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-833-790-413

Query Match 99.6%; Score 3230; DB 9; Length 632;
Best Local Similarity 99.7%; Pred. No. 9.7e-257;
Matches 630; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDTMMMLNVRNLFEQLVVRVLESEGNEVQFQLAKOFEDEFRKKWQRTDHEGKYKULMK 60

Db 1 MDTMMMLNVRNLFEQLVVRVLESEGNEVQFQLAKOFEDEFRKKWQRTDHEGKYKULMK 60

QY 61 AFTERSALDVKLUKHARNQVDVTKRORAEADCEKLERQIOLIREMIMCDTSQIOLSEE 120

Db 61 AFTERSALDVKLUKHARNQVDVTKRORAEADCEKLERQIOLIREMIMCDTSQIOLSEE 120

QY 121 OKSALAFLNRCOPSSNAGNKLSTIDESGSLSDSFDKDDESLDWDSSILVTKFLKKR 180

Db 121 OKSALAFLNRCOPSSNAGNKLSTIDESGSLSDSFDKDDESLDWDSSILVTKFLKKR 180

QY 181 EKRSTSRQFVQDGPGPVKKRSIGSAVDQGENESIVAKTTVNPNGGPRAVSTETVP 240

Db 181 EKRSTSRQFVQDGPGPVKKRSIGSAVDQGENESIVAKTTVNPNGGPRAVSTETVP 240

QY 241 YWTRSRRKRTGTLQPNWSDSTLNSRQLEPRTEDSVGTPQSONGMRHDFVSKTVKRESC 300

Db 241 YWTRSRRKRTGTLQPNWSDSTLNSRQLEPRTEDSVGTPQSONGMRHDFVSKTVKRESC 300

QY 301 VPGCKRTRFGKLSIKCRDCRVPVSHPECRDRCPCLPCITPLGTPVKIGEGMLADPVQSTSP 360

Db 301 VPGCKRTRFGKLSIKCRDCRVPVSHPECRDRCPCLPCITPLGTPVKIGEGMLADPVQSTSP 360

QY 361 MIPSIWVHCWNEIEQRGTTGKLRISGCDRTVKELEKFLAVKTVPLLSKUDHAIICS 420

Db 361 MIPSIWVHCWNEIEQRGTTGKLRISGCDRTVKELEKFLAVKTVPLLSKUDHAIICS 420

QY 421 LKDFLFLNKLKEPLTFRNRAFMEAETTDEDSNIAAMYQAVGELPOANRDTAFLMHL 480

Db 421 LKDFLFLNKLKEPLTFRNRAFMEAETTDEDSNIAAMYQAVGELPOANRDTAFLMHL 480

QY 421 LKDFLFLNKLKEPLTFRNRAFMEAETTDEDSNIAAMYQAVGELPOANRDTAFLMHL 480

Db 421 LKDFLFLNKLKEPLTFRNRAFMEAETTDEDSNIAAMYQAVGELPOANRDTAFLMHL 480

QY 481 ORVAQSPHTKMDVANLAKVFGPTIVAHAVNPDPVMSQDIKRQPKVVERLISLPLEWWS 540

Db 481 ORVAQSPHTKMDVANLAKVFGPTIVAHAVNPDPVMSQDIKRQPKVVERLISLPLEWWS 540

QY 541 QPMVEQENTIDPLHVENSNASTPQDPKISLGLGVTTEHQQLKTPSSSSLQVRVS 600

Db 541 QPMVEQENTIDPLHVENSNASTPQDPKISLGLGVTTEHQQLKTPSSSSLQVRVS 600

QY 601 TLTQNTRPRFGSKSKSATNLGROGNFFASPMLK 632

Db 601 TLTQNTRPRFGSKSKSATNLGROGNFFASPMLK 632

RESULT 3
US-09-833-790-427
; Sequence 427, Application US/09833790
; Patent No. US-0020068288A1

GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Indrias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 427
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-833-790-427

Query Match 90.0%; Score 2919; DB 9; Length 570;
Best Local Similarity 99.8%; Pred. No. 3.4e-231;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 63 TERSALDVKLUKHARNQVDVTKRORAEADCEKLERQIOLIREMIMCDTSQIOLSEEQK 122

Best Local Similarity 99.2%: Pred. No. 1e-88; Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 397 KERKFLRKYTVPLISKVVDIHAICCSLUKDPLRNLKEPLTRFLRNLRAFMEAAITDEDSIA 456
Db 20 KUKFLRLRKYTVPLISKVVDIHAICCSLUKDPLRNLKEPLTRFLRNLRAFMEAAITDEDSIA 79
QY 457 AMYQAVGELPQANRDTAFLMILHQRYAQSPHTKMDVANLAKVFGPTIVAHVPNPDPT 516
Db 80 AMYQAVGELPQANRDTAFLMILHQRYAQSPHTKMDVANLAKVFGPTIVAHVPNPDPT 139
QY 517 MSQDIKQPKVVERLISPLLEWSQFMNVEQEIQNIDPLHVIENSAFTSPQDPDIKSLG 576
Db 140 MLDIKQPKVVERLISPLLEWSQFMNVEQEIQNIDPLHVIENSAFTSPQDPDIKSLG 199
QY 577 PVTPEHQLKTPSSSSLSQVRSTLTKNTPRFGSKSKSATNLGROONFPASPMLK 632
Db 200 PVTPEHQLKTPSSSSLSQVRSTLTKNTPRFGSKSKSATNLGROONFPASPMLK 255

RESULT 6
US-09-881-736-6
; Sequence 6, Application US/09881736
; Patent No. US20020076785A1
; GENERAL INFORMATION:
; APPLICANT: Glotzer, Michael
; APPLICANT: Jantsch-Plunger, Verena
; APPLICANT: Romano, Aiper
; APPLICANT: Mishina, Masanori
; APPLICANT: Kaitna, Susanne

TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their use in screening methods
FILE REFERENCE: 0552.2266001/1EKS/AES
CURRENT APPLICATION NUMBER: US/09/881-736
PRIORITY APPLICATION NUMBER: EP 00 112 880.0
PRIORITY FILING DATE: 2000-06-19
PRIORITY NUMBER: EP 01 110 554.1
FILING DATE: 2001-04-30
PRIORITY APPLICATION NUMBER: 60/241,231
PRIORITY FILING DATE: 2000-10-18
PRIORITY NUMBER: To be determined
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 681
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans

Query Match 16.7%; Score 541.5; DB 9; Length 681;
Best Local Similarity 25.9%; Pred. No. 2.6e-5;
Matches 180; Conservative 109; Mismatches 285; Indels 121; Gaps 22;

QY 7 NYTNLFFQOLVRVEILSEGNEVQFIOLAKDFFDRKQW-----ORTDHLSGKYDLM 59
Db 14 NSRHFNMWLNSSORPQFDIKIDGMFLHLDTEIRLRLKWLDSBESKRNLADMRABALA 73
Qy 60 KAETERSALDVKLKHARNQVWEIKRQORAEADCEKLERQIOLIREMLMCITGSGTQLE 119
Db 74 KARKKLAMPFDIVKDTQKHLRAMEENKALKLNUVETRERQKOLKDAMKGIFNS-LTK 131
Qy 120 EOKSALAFNLRGQPSNSNAGNAVGKRRSASAHITAAMANSRSRVRTATIDEEPNEGGTPKR 176
Db 132 EUDQDFKELHE--PLRTYSKRVO- ORHPHIMEDQDDPDESDVYDGTGDSFEEVH 186
Qy 177 LKK-REKRSTS-----RQFDGPRG---PVKK 200
Db 187 LKNGREVRSSAAGNAVGKRRSASAHITAAMANSRSRVRTATIDEEPNEGGTPKR 246
Qy 201 TTSIGSAVQGNEISIVAKTTV-----VPMQCGP-----IEAVSTIETVP 240

RESULT 7
US-10-408-765A-598
; Sequence 598, Application US/10408765A
; Publication No. US200401010874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Sounmitra S.
; APPLICANT: Faby, Boin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: PatSeqQ for Windows Version 4.0
SEQ ID NO 598
LENGTH: 2022
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-408-765A-598
Query Match 10.3%; Score 334; DB 16; Length 2022;
Best Local Similarity 23.0%; Pred. No. 1.7e-17;
Matches 147; Conservative 111; Mismatches 26; Indels 116; Gaps 26;

Qy 22 LSEBGNEQ-----FIOLAKDFFDRKQW--RTDHLSGKYDLMKETERSALDV 70
Db 1404 LSPGSQDSKSTPKFLRFLHKYD---KXSYLEGAELEENAVSGHVLBATTMKGLEA 1458
Qy 71 -----KUJHARNOVDEVKRQORAEADCEKLERQIOLIREMLMCITGSGTQLE 126
Db 1459 PSGQHKAAGE-----KRTKEPGGKKGKRNVKI-----GKTVSEKRSVF 1502
Qy 127 FLARQGQPSNSNAGNAVGKRRSASAHITAAMANSRSRVRTATIDEEPNEGGTPKR 185
Db 1503 -----RQITNAN---EIKYIIDEFLANKINDLRSOKTP-----IESLFIATEKFRS 1545
Qy 186 TSQFVGDGPVVKKTRTSIGSAVQGNEISIVAKTTV-----VPMQCGP-----IEAVSTIETVP 240

PRIOR FILING DATE: 2001-01-30 ; APPLICANT: Lepley, Denise M.
; PRIOR APPLICATION NUMBER: 60/265,514 ; APPLICANT: Rieger, Daniel K.
; PRIOR FILING DATE: 2001-01-31 ; APPLICANT: Burges, Catherine E.
; PRIOR APPLICATION NUMBER: 60/265,517 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; PRIOR FILING DATE: 2001-01-31 ; FILE REFERENCE: 21402-258
; PRIOR APPLICATION NUMBER: 60/265,412 ; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2001-01-31 ; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,395 ; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-31 ; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,406 ; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-02-02 ; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,767 ; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-02-05 ; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/267,057 ; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-02-07 ; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,975 ; PRIOR APPLICATION NUMBER: 60/265,406
; PRIOR FILING DATE: 2001-02-07 ; PRIOR FILING DATE: 2001-02-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391 ; PRIOR APPLICATION NUMBER: 60/267,057
; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO: 879
; LENGTH: 175 ;
; TYPE: PRT ;
; ORGANISM: Artificial Sequence ;
; FEATURE: ;
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: GTPase-activator protein for Rho-like GTPases
; US-10-072-012-879
; Query Match 9.9%; Score 322; DB 15; Length 175;
; Best Local Similarity 45.1%; Pred. No. 3 7e-18; Mismatches 64; Indels 6; Gaps 3;
; Matches 78; Conservative 25; MisMatches 64; Indels 6; Gaps 3;
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; Qy 362 TSIIVHCVNELEBQRGLTETGLYRISGCDRTKELKPKLRLKTVPLSKVVDIATCSL 421 ;
; Db 3 IPIIVKCIETYLEKRGDTEGTYRKSGSASRYKELRAFDGSPDPDLDSEYDVHDVAGL 62 ;
; Qy 422 IKFDFLRNLKEPLTFRNRAFMEAETDEDSNIAAMQAVSPLQANRDTIAFLMTHLQ 481 ;
; Db 63 IAKFLRSLPEPITFELYEEFBAAKLDEDEERLRARELSSLPANRATYLLAHN 122 ;
; Qy 482 RYAQ-SPTKMDVANLAKYFGPTIVAHAVNPNDPVMTS-QDIKRQPKVVERLU 532 ;
; Db 123 RVAEHSSENKMARNLAIIVFGPLUR---PPDGESASLKDRIKHONKVVELI 171 ;
;
; RESULT 10 ;
; US-10-072-012-733
; Sequence 733, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar ;
; APPLICANT: Spytek, Kimberly ;
; APPLICANT: Zerhuren, Bryan ;
; APPLICANT: Patturajan, Meera ;
; APPLICANT: Shimkebs, Richard ;
; APPLICANT: Li, Li ;
; APPLICANT: Gangoli, Ezra ;
; APPLICANT: Radigaru, Muralidhara ;
; APPLICANT: Anderson, David W. ;
; APPLICANT: Rastelli, Luca ;
; APPLICANT: Miller, Charles E. ;
; APPLICANT: Gerlach, Valerie ;
; APPLICANT: Taupier Jr, Raymond J. ;
; APPLICANT: Gusev, Vladimir Y. ;
; APPLICANT: Colman, Steven D. ;
; APPLICANT: Wolenc, Adam R. ;
; APPLICANT: Pena, Carol E. A. ;
; APPLICANT: Furtak, Katarzyna ;
; APPLICANT: Grosse, William M. ;
; APPLICANT: Alsobrook II, John P. ;
; LENGTH: 1261 ;
; TYPE: PRT ;
; ORGANISM: Homo sapiens ;
; SEQ ID NO: 733 ;
; LENGTH: 1261 ;
; TYPE: PRT ;
; ORGANISM: Homo sapiens ;
; US-10-072-012-733
; Query Match 9.6%; Score 310; DB 15; Length 1261;
; Best Local Similarity 21.8%; Pred. No. 7.9e-16; Mismatches 269; Indels 136; Gaps 27;
; Matches 146; Conservative 119; MisMatches 269; Indels 136; Gaps 27;
;
; Qy 182 KRSTSRQFVDPGPPGPKRTRSIGSAVQDGNESTIVAKTTVTPVNDGQPIEAUSTIETVY 241 ;
; Db 372 RRLLEEAQKV--EANELYKV-CVTVNEERNDLIENTKELIAQLRILVQCDLILKA 427 ;
; Qy 68 LDVKLKHARNQDVKEKRRQRAEADCKELEKQIQLRREMIDTSQSIQSEEQK--SA 124 ;
; Db 428 VTVNLFFMHOQLAASLDSLQSLCDSAKLYPDQGQBYSEFVKATNS---TEBEKVQGV 482 ;
; Qy 125 LAFLNRQGQPSSENAGKRLSTI--DESGSLISDSDFKIDESLWDSLSSLUVKLKKRE 181 ;
; Db 483 NGHLNSQPSGSGPANSLEDVRLPDSKNEEDCNSADIT--GPSFIRSWTFGMFS 539 ;
; Qy 182 KRSTSRQFVDPGPPGPKRTRSIGSAVQDGNESTIVAKTTVTPVNDGQPIEAUSTIETVY 241 ;
; Db 540 DSEST-----GSESRSLDS-----ESI-----SPGD----- 562 ;
; Qy 242 WTRSRRTKGCTQWPNSTNSQLERPTT--DSVGTPOQ--NGGMRLLHDVSKTVIK 296 ;
; Db 563 FHRKLRTTPSSGTMSSADDLDRREPPSPSETGPNSLGTFKTLMSKALTHKF--RKLRS 620 ;
; Qy 297 PESCVPGKPKGKSLKCDRVSHPSPDRCPCLPFLIGPKGEGMADPV 356 ;
; Db 621 PTKRCREGIVF--QGVECEBCLVCHRKLLENVLICGKOKLCKTHGAFTQVAK 678 ;
; Qy 357 OTSPMISIVHCVNELEBQRGLTETGLYRISGCDRTKELKPKLRLKTVPLSKV-- 413 ;
; Db 679 KEPDGPIPKCASEBNRACILOGIYVG-------NKTKTEKQALEGM 726 ;
; Qy 414 ---DI----HAICSLKDFLRNLKEPLTFRNRAFMEAETDEDSNIAAMQAVSPLQANRDTIAFLMTHLQ 454 ;
; Db 727 HLVDISHSSHDICDVLKLYLROLBPFILRFLYKEFDLAKETOHNEEOETKNSLED 786 ;
; Qy 455 -----IAAMQAVSPLQANRDTIAFLMTHLQVA-QSPHTKMDVANLAKV 500 ;

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Db 787 KKPWNCIEINRILKSKDLRQLPASNFSNLHFLIVKRVDHABENKNSKNLGVIF 846
Qy 501 GPTIVAHAVNPUPUTMSQ--DTRKQPKVERULSLPLEYWSQFM---MVEQENTIPHLH 554
Db 847 GTSLLI--RERPTAPITSSLABTSNQARLTS--VYSKIFDGSLSQDPMWSIG 900
Qy 555 VIENS--NAFSTPQTPIKVSLGPPVTPBEHOLKTPSSSSLSQRVSTLTQNTPRFGS 611
Db 901 VWDQGCFPKPLLSPEERDERSMSKSLFSSKEDIHTSESESKIFERAT--FEE 952
Qy 612 KSKSATNLGR 621
Db 953 SERKONALGK 962

RESULT 11
US-10-177-980-2
; Sequence 2, Application US/10177980
; Publication No. US2003016623A1
; GENERAL INFORMATION:
; APPLICANT: Saras, Jan
; APPLICANT: Franzn, Petra
; APPLICANT: Aspenskrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Gonza, Leonel Jorge
; APPLICANT: Heldin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
; FILE REFERENCE: L0461/030
; CURRENT APPLICATION NUMBER: US/10/177,980
; CURRENT FILING DATE: 2002-06-21
; PRIORITY NUMBER: US/09/080,855
; PRIORITY FILING DATE: 1998-05-18
; PRIORITY APPLICATION NUMBER: 08/805,583
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 2
; LENGTH: 1261
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-177-980-2

Query Match 9.3%; Score 301; DB 14; Length 1261;
Best Local Similarity 22.4%; Pred. No. 4.3e-15;
Matches 153; Conservative 120; Mismatches 249; Indels 160; Gaps 33;
Qy 9 RNLFEQLVRRVTEILSENEVQFOLAKDFEDFRKKWQRTDHE-LGKYKDLMLKAETRSA 67
Db 372 RLEEEALQKVE--BADELYK-VCVTNEVERRNDVENTKRELAQRTLVFOCDLTKA 427
Qy 68 LDVYKLKHARNQDVTEIKRORABADCEKLERQIOLIREMLMCDTGSSTQLSRQK--SA 124
Db 428 VTVNLFLPHQQLQASLADRQLSCLGSAKLYDPQBYSEPVKATNS---TBEKVQGNV 482
Qy 125 LAFLNRGQPSNSNAGNRLSTI--DEGSQILSDISFDKTDLSLDWDSLVLVTPKLUKRE 181
Db 483 NKLHNSSQPSGRGPANSLEDVVRLPDSNSNKIBEDRCNSADIT--GPSFIRSWTGMFS 539
Qy 182 KRSTSTROFVDDGGPGPVKRTSISAVDQGNESIVAKTTVTPNDGGPIEAVSTIETPY 241
Db 540 DSEST-----GSSSESRLSDS-----ESI-----SPGD----- 562
Qy 242 WTRSRKRTGLOPWNSTNSKOLRERPTT--DSVGTPOS--NGGMRLLDHFVSKTVK 296
Db 563 FHRKLPLRPTPSGTMSSADDLDEREPPSPSETGNSLIGFKTLMKAALTHKE--RKLRS 620
Qy 297 PSCCVPGKRIKGKLSKCRDCRVSHPECRDCPLC---IP---TLLGTPVKIGEG 349
Db 621 PTKCRDCBGIIVVF--QGVECECLVCHRKCLENLVICGHQKLPGKIHFG----- 670
Qy 350 MLADP--VSQTP--MIPSIVHCVNEBORGLTETGLYKRISSGDRTYKELKEKFLRKT 406

RESULT 12
US-10-648-93-192
; Sequence 192, Application US/10648593
; Publication No. US2004010613A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D02473 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIORITY NUMBER: 60/406,385
; PRIORITY FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 192
; LENGTH: 1261
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-648-593-192

Query Match 9.3%; Score 301; DB 16; Length 1261;
Best Local Similarity 22.4%; Pred. No. 4.3e-15;
Matches 153; Conservative 120; Mismatches 249; Indels 160; Gaps 33;
Qy 9 RNLFEQLVRRVTEILSENEVQFOLAKDFEDFRKKWQRTDHE-LGKYKDLMLKAETRSA 67
Db 372 RLEEEALQKVE--BADELYK-VCVTNEVERRNDVENTKRELAQRTLVFOCDLTKA 427
Qy 68 LDVYKLKHARNQDVTEIKRORABADCEKLERQIOLIREMLMCDTGSSTQLSRQK--SA 124
Db 428 VTVNLFLPHQQLQASLADRQLSCLGSAKLYDPQBYSEPVKATNS---TBEKVQGNV 482
Qy 125 LAFLNRGQPSNSNAGNRLSTI--DEGSQILSDISFDKTDLSLDWDSLVLVTPKLUKRE 181
Db 483 NKLHNSSQPSGRGPANSLEDVVRLPDSNSNKIBEDRCNSADIT--GPSFIRSWTGMFS 539
Qy 182 KRSTSTROFVDDGGPGPVKRTSISAVDQGNESIVAKTTVTPNDGGPIEAVSTIETPY 241
Db 540 DSEST-----GSSSESRLSDS-----ESI-----SPGD----- 562
Qy 242 WTRSRKRTGLOPWNSTNSKOLRERPTT--DSVGTPOS--NGGMRLLDHFVSKTVK 296
Db 563 FHRKLPLRPTPSGTMSSADDLDEREPPSPSETGNSLIGFKTLMKAALTHKE--RKLRS 620
Qy 297 PSCCVPGKRIKGKLSKCRDCRVSHPECRDCPLC---IP---TLLGTPVKIGEG 349
Db 621 PTKCRDCBGIIVVF--QGVECECLVCHRKCLENLVICGHQKLPGKIHFG----- 670

```


Matches	154;	Conservative	111;	Mismatches	258;	Indels	125;	Gaps	25;
Qy	8	VRLFELQOLVRRVLELSEGNEVQPIOLAKDFEDRKKW	-----	-----	-----	-----	-----	-----	54
Db	43	LRMLEDESRMENASE	-----	-----	-----	-----	-----	-----	95
Qy	55	KDLIMKATERSALDVKUHARNQDVDEBKKRRAEADCEKUBRQIQIUREMIMCDTSGS	-----	-----	-----	-----	-----	-----	114
Db	96	KHLNLSSKKES	-----	-----	-----	-----	-----	-----	140
Qy	115	IQSEEQISALATL	-----	-----	-----	-----	-----	-----	167
Db	141	:-KMFEPVPLAFLQGLMPYHGYELAKDFGDFKTL	-----	-----	-----	-----	-----	-----	190
Qy	168	DSSLVKPFKKKE	--KRSRISRSQFVIGPGPVKKTSGSAVDQGNESTIAKTTTVP	-----	-----	-----	-----	-----	224
Db	191	TRSEVESLMMKKMENPLSHKTISPYTMGYL	-----	-----	-----	-----	-----	-----	241
Qy	225	NDGGPIEAVSTIEVPMRSTRKRTGTLQPMWNSDTSNRSQLEPRTEDSVGPSONGGM	-----	-----	-----	-----	-----	-----	284
Db	242	RDS	-----	-----	-----	-----	-----	-----	280
Qy	285	RLIDFVSKVTKIBESCVPGKRIKFGKUSIKCPCDCRUVSHPSCTRDRCLPCPTLICPV	-----	-----	-----	-----	-----	-----	344
Db	281	KRCFCPDVEAVDRGVITMQLSBDRLWMEAMDGEPVNNSRD	-----	-----	-----	-----	-----	-----	325
Qy	345	KLGEGLADFVFSQTSQPMPSIVHCVNIEQRLTETGTYRISGCDRTVKEJKEKFLRVK	-----	-----	-----	-----	-----	-----	404
Db	326	SQSEG	-----	-----	-----	-----	-----	-----	380
Qy	405	TVPLSKVD	-----	-----	-----	-----	-----	-----	457
Db	381	AA	--SETETDICAWEWEIKTIVSALKYIYRMLRGPLMMYQFORSFIKAKLENQETRVE	-----	-----	-----	-----	-----	437
Qy	458	MYQAVGELPQANRDTLATLIMHILQVAVS	-PRTKMDVANLAKUFGPTIVAHAVPNPPVT	-----	-----	-----	-----	-----	516
Db	438	IHSVHLRPLKORQMLQMLNHLANVANH	KONLMTVANGUVFGPTLIR	--	-----	-----	-----	-----	494
Qy	517	MSODIKRPRVVERLLSLISPLEYSQFMNVEQENIDPLHVNENSNAPSTPQT	-PDIKVSL	-----	-----	-----	-----	-----	575
Db	495	AIMDIKQNTIVBILLENHEKLFNTVPDVPLTNAQ	-IHLRKSSDSKPPGSKRSATNL	-----	-----	-----	-----	-----	553
Qy	576	GPVTPERQ	--LHKTPSSSSISQVRSTLTQNTPRFGSKRSATNL	-----	-----	-----	-----	-----	619
Db	554	HAVPSTERKOEORNINSISSLSESVSSANSISSLQPNLNSSDSNL	-----	-----	-----	-----	-----	-----	601

Search completed: February 1, 2005, 14:23:09
 Job time : 148 secs

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Li/R 736
Seq. ID 2

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 1, 2005, 13:56:16 ; Search time 164 Seconds
(without alignments)
1382.420 Million cell updates/sec

Title: US-09-881-736A-2

Perfect score: 3243

Sequence: 1 MDTMLMLNVRNLFEQLWRRVE..... SKSATNLGROGNFFASPMLK 632

Scoring table: BL0STIM62
Gapext 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq 23Sep04:*

1: geneseqD1980s:*

2: geneseqD1990s:*

3: geneseqD2000s:*

4: geneseqD2002s:*

5: geneseqD2003as:*

6: geneseqD2003bs:*

7: geneseqD2003bs:*

8: geneseqD2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	3237	99.8	632 4	ABU53065
2	3237	99.8	632 7	AD60209
3	3237	99.8	632 7	ADP5165
4	3237	99.8	632 8	ADP0214
5	3233	99.7	632 4	ADM0047
6	3230	99.6	632 5	AuU9419
7	2919	90.0	570 5	AU69422
8	2734	84.3	628 7	AD60207
9	1182	36.4	255 4	ABG4223
10	1182	36.4	255 7	ADJ9239
11	971.5	30.0	256 4	ADU32069
12	864	26.6	625 4	ABR8056
13	625	19.3	4318 4	ABG14787
14	618	19.1	665 4	ABG1230
15	618	19.1	1086 4	ABG19904
16	178	19.1	1139 4	ABG13958
17	581	17.9	119 4	Aam41833
18	477	14.7	384 4	ABG59247
19	334	10.3	2022 7	ADJ68792
20	323.5	10.0	1240 6	ABR1659
21	323.5	10.0	2158 7	ADD18702
22	322	9.9	175 5	ADJ17343
23	322	9.9	175 5	ADJ17342
24	322	9.9	334 4	AMM9659
25	322	9.9	4	AAM41445

ALIGNMENTS				
RESULT 1	ABU53065	ID	ABU53065	standard; protein; 632 AA.
XX	XX	AC	ABU53065;	
XX	XX	DT	14-APR-2003 (first entry)	
XX	XX	DE	Human signal transduction-associated protein from DKFZphtes3_1cl.	
XX	XX	KW	Human; gene therapy; vaccine; disease treatment; detection.	
XX	XX	OS	OS	
XX	XX	PN	PN	
XX	XX	PF	PF	
XX	XX	PR	PR	
XX	XX	PR	18-AUG-1999; 99US-01565U3P.	
XX	XX	PR	28-SEP-1999; 99US-01565U3P.	
PA	PA	PI	(GHU-) GERMAN HUMAN GENOME PROJECT.	
XX	XX	PI	Wiemann, S;	
XX	XX	DR	WPI; 2001-327840/34.	
DR	DR	DR	N-PSDB; ABX71357.	
XX	XX	PT	Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.	
CC	CC	PT	This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a polypeptide described in the disclosure of the invention.	
CC	CC	CC	Sequence 632 AA;	
CC	CC	CC	Sequence 632 AA;	

DT 12-AUG-2004 (first entry)
 XX
 DE Human PRO polypeptide #559.
 XX
 KW Human; PRO; immune related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
 KW XX
 OS Homo sapiens.
 XX
 PN WO2004043361-A2.
 XX
 PD 27-MAY-2004.
 XX
 PP 06-NOV-2003; 2003WO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;
 XX
 DR WPI; 2004-420067/39.
 XX
 PT Novel PRO polypeptide e.g., PRO69614, PRO71105, or PRO86388 useful for treating an immune related disorder, such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or spondyloarthropathy.
 XX
 PS Claim 7; SEQ ID NO 1118; 1731PP; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polypeptide of the invention.
 CC
 CC Sequence 632 AA;
 XX
 SQ Query Match 99.8%; Score 3237; DB 8; Length 632;
 Best Local Similarity 99.8%; Prod. No. 2.2e-263; Matches 631; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDTMLNTRNLFEQLVVRVVEILSEGNEVQFQLAKDFDFRKWQRTDHEGKXKDJLMK 60
 DB 1 MDTMLNTRNLFEQLVVRVVEILSEGNEVQFQLAKDFDFRKWQRTDHEGKXKDJLMK 60
 QY 61 AETERSALDVKJLKHARNQDVDEIKRRAEADCEKLERQIOLIREMLMCDSQIOLSEE 120
 DB 61 AETERSALDVKJLKHARNQDVDEIKRRAEADCEKLERQIOLIREMLMCDSQIOLSEE 120
 QY 121 QKSALAFNRRGQPSWAGNKRUSTIERSGSLSDISFDKTBLSLMDSSLLVTKLKKR 180
 DB 121 QKSALAFNRRGQPSWAGNKRUSTIERSGSLSDISFDKTBLSLMDSSLLVTKLKKR 180
 QY 181 EKRSTTSRQFVQGPPGPVKKTSIGSAVQGNESIVAKTTVTPNDGGPTEAVSTIETVP 240
 DB 181 EKRSTTSRQFVQGPPGPVKKTSIGSAVQGNESIVAKTTVTPNDGGPTEAVSTIETVP 240
 DR N-PSDB; AAI59203.
 XX
 QY 241 YWTRSRKRTGQLQPMNSDTSNRLQPEPRTDSVGTQPSNGMRLHDYFVSKTVEPSC 300
 DB 241 YWTRSRKRTGQLQPMNSDTSNRLQPEPRTDSVGTQPSNGMRLHDYFVSKTVEPSC 300
 QY 301 VPGKIKIFGKLSKRCRDCRVSHPBCRDRCLPCTPLTIGPVKIGEGLADFVSQTP 360
 DB 301 VPGKIKIFGKLSKRCRDCRVSHPBCRDRCLPCTPLTIGPVKIGEGLADFVSQTP 360
 QY 361 MIPSIWVHCVNBIEQRLGTERGLYRISGCDRTVKELKEFLRKVYVFLSKDDHAICS 420
 DB 361 MIPSIWVHCVNBIEQRLGTERGLYRISGCDRTVKELKEFLRKVYVFLSKDDHAICS 420
 QY 421 LKDFKFLNKEPLLTFRNRAFMEAJEITDNDSLAMYQAVGELQCAQRDQFLAFMHL 480
 DB 421 LKDFKFLNKEPLLTFRNRAFMEAJEITDNDSLAMYQAVGELQCAQRDQFLAFMHL 480
 QY 481 ORVAQSPHTKQDVKANLAKVQKPTIVAHAVRNPDPVMSQDKRQPKVVERLISPLEWYS 540
 DB 481 ORVAQSPHTKQDVKANLAKVQKPTIVAHAVRNPDPVMSQDKRQPKVVERLISPLEWYS 540
 QY 541 QFMVVEQBNIDPLHVENSNAFSTPQTDIKUSLQGPVTPERQLIKTPSSLSORVRS 600
 DB 541 QFMVVEQBNIDPLHVENSNAFSTPQTDIKUSLQGPVTPERQLIKTPSSLSORVRS 600
 QY 601 TLTKNTRPFGSKSKSATNLGRQGNFPASPMK 632
 DB 601 TLTKNTRPFGSKSKSATNLGRQGNFPASPMK 632
 DR N-PSDB; AAI59203.

RESULT 5
 XX
 DE Human polypeptide SEQ ID NO 3192.
 XX
 ID AAM40047 standard; protein; 632 AA.
 XX
 AC AAM40047;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 3192.
 XX
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chomatotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.
 KW XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US034263.
 XX
 PR 23-DEC-1999; 99US-0047725.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-0055317.
 PR 20-JUN-2000; 2000US-0059842.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-0065450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-0069336.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D, Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI; 2001-442253/47.
 DR N-PSDB; AAI59203.

PT Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

PT

XX

RS

XX

CC

XX ADB60207; standard; protein; 628 AA.
 XX AC
 XX DE
 XX DT 29-JAN-2004 (first entry)
 XX XX Rat; protein AAH10715, SEQ ID NO 6113.
 XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX OS Rattus norvegicus.
 XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX DR 01-NOV-2001; 2001US-0346382P.
 XX PR 26-NOV-2001; 2001US-0333347P.
 XX PA (GRHO) GEN HOSPITAL CORP.
 PA (FARR) BAYER AG.
 XX PI Woolf C, D'urso D, Beffort K, Costigan M;
 XX WPT; 2003-268312/26.
 DR GENBANK; AAH10715.
 XX PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
 XX PS Claim 1, Page: 101pp; English.
 XX CC The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification), which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at http://wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 628 AA;

QY 60 KASPTERSALDVULKHARNQVDEIKRQRRAEADCEKLERQQTQIREMMDPSGSIOLSE 119
 QY 61 KASPTERSALDVULKHARNQVDEIKRQRRAEADCEKLERQQTQIREMMDPSGSIOLSE 120
 QY 120 EQKSLATLNRGQPSSSAGNRLSTDESGSILSDISFDKQDESLWDSSVJVKFLKK 179
 QY 121 EQKSLATLNRGQPSSSAGNRLSTDESGSILSDISFDKQDESLWDSSVJVKFLKK 180
 QY 180 REKRSRSTROFGVPPGRVKRSIGSVAQDNESTVAKTTVPNQGPIBAVSTETV 239
 QY 181 REKRSRSTROFGVPPGRVKRSIGSVAQDNESTVAKTTVPNQGPIBAVSTETV 240
 QY 240 PYWTRSRKRTGICQPMNSDSTNSQLEPRTSTDVGVTQPSQSGMLRHDPYFVSKTVKPS 299
 QY 241 PSWTRSRKSGPLQPVNSDANSRPLPRTSTDVGVTQPSQSGMLRHDPYFVSKTVKPS 300
 QY 300 CVPGCKR1KFGKUSLKCRDCR1VSHPECRDRPLCPLCPTLICPTVPLK1GEGM1ADFVSQTS 359
 QY 301 CVPGCKR1KFGKUSLKCRDCR1VSHPECRDRPLCPLCPTLICPTVPLK1GEGM1ADFVSQTS 360
 QY 360 PMPSP1VHCVNTEQORSLTETGYLRSGCDPRTYKELKEKEFVTKWPLSKVDDHAIC 419
 QY 361 PMPA1IVVSCVNLIEQRG1TEAQLYR1SGCDR1VKEKEFVTKWPLSKVDDHAIC 420
 Db 420 SLIKDFLRNLKEPILTFRLNRAFMARITDENSIAAMQAVGELPOANRDLAFLMH 479
 Db 421 SLIKDFLRNLKEPILTFRLNRAFMARITDENSIAAMQAVGELPOANRDLAFLMH 480
 QY 480 LORVAQSPHTKMOVANLAKVFGPTVIAHAPVDPVPMQSQD1KRPQKVVERLISLPLBHY 539
 QY 481 LORVSQSPDTKMDIANLAKVFGPTVIAHAPVDPVPMQSQD1KRPQKVVERLISLPLBHY 540
 QY 540 SQTMAVEQENIDLHVENSASFSTPQTDKIVSLGQPTTBHQJLKTQSSLSQRV 599
 QY 541 NQFMWQDNEIDS---ORGNSTPRTDVKVSLGQPTTBHQJLKTQSSLSQRV 596
 Db 600 STLTKNTRPFGSKSATNLGQGNFFASPMK 632
 Db 597 N-LSKSTPRFGNSKSATNLGQGKFFFAPYLUK 628
 RESULT 9
 AAB94223 ID AAB94223 standard; protein; 255 AA.
 AC AAB94223;
 XX DT 26-JUN-2001 (first entry)
 XX DE Human protein sequence SEQ ID NO:14587.
 XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 XX OS Homo sapiens.
 XX PN EP1074617-A2.
 XX PD 07-FEB-2001.
 XX PR 28-JUL-2000; 2000EP-00116126.
 XX PR 29-JUL-1999; 99JP-00248036.
 PR 11-JAN-2000; 2000JP-00118776.

Query Match	84.3%	Score	2734	DB	7	Length	628
Best Local Similarity	84.4%	Pred.	No. 5	6e-221			
Matches	534;	Conservative	47;	MinMatches	421	Indels	6;

PR	31-MAR-2000; 2000US-00540217.
DR	23-AUG-2000; 2000US-00649167.
XX	(HYSE-) HYSEQ INC.
XX	Drmanac RT, Liu C, Tang YT;
XX	WPI: 2001-639362/73.
XX	N-PSDB; AAS74417.
PT	New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
PT	Claim 20; SEQ ID NO 40589; 103pp; English.
CC	The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The patient did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
CC	Sequence 665 AA;
CC	Query Match 19.1%; Score 618; DB 4; Length 665;
CC	Best Local Similarity 46.9%; Pred. No. 1.4e-42;
CC	Matches 153; Conservative 35; Mismatches 68; Indels 70; Gaps 11;
CC	Sequence 665 AA;
QY	255 WNSDSTLNSRQLEPRTETDVGTPQSNGMRLHDVFSKTKVTPKESCPGKRIKGKLSL 314
DB	369 WIKD-LNVRKPTKTKLEENIGNTIQDINGK-KDMSKT--PKAMATTKDKWDLILQ 422
QY	315 KCRDCRVSHPBCRDRCPPLCPICTLIGTPVKIG---EGMLADFVQSQTSPMIPSIVH 368
DB	423 KSFFC-----TAKETTIRVNROPTEWKIFATVSSD----KGJISR 459
QY	369 CVNETEQ-----RLGTTGGLY---RISGCDR--TVKELKEK-FLRV 403
DB	460 IYNELKQIYKKKTNPIKWTNDMMRHSKEDIYAAKKHMKCCSSLPAIREMQIKTMY 519
QY	404 KTVPLI-----SKVDIHAISLKLQPLNLKEPLIFPRLNAAFMEAETBDN 453
DB	520 HLTPPIRATIILKKSGNNKVDIHAISLKLQPLNLKEPLIFPRLNAAFMEAETBDN 579
QY	454 SIAMMQAVGELPQARDTIAFLMILHQVRQAVSPHTKMDVANLAKVQPTIVAHAVNPD 513
DB	580 SISAMMQAVGELPQARDTIAFLMILHQVRQAVSPHTKMDVANLAKVQPTIVAHAVNPD 639
QY	514 PVTMMSDIIKQPKPQVKVERLILSIPLEYW 539
DB	640 PVTMMSDIIKQPKPQVKVERLILSIPLEYW 665
XX	Sequence 1086 AA;
CC	Query Match 19.1%; Score 618; DB 4; Length 1086;
CC	Best Local Similarity 46.9%; Pred. No. 3.2e-42;
CC	Matches 153; Conservative 35; Mismatches 68; Indels 70; Gaps 11;
CC	Sequence 1086 AA;
QY	255 WNSDSTLNSRQLEPRTETDVGTPQSNGMRLHDVFSKTKVTPKESCPGKRIKGKLSL 314
DB	790 WIKD-LNVRKPTKTKLEENIGNTIQDINGK-KDMSKT--PKAMATTKDKWDLILQ 843
QY	315 KCRDCRVSHPBCRDRCPPLCPICTLIGTPVKIG---EGMLADFVQSQTSPMIPSIVH 368
DB	844 KSFFC-----TAKETTIRVNROPTEWKIFATVSSD----KGJISR 880
QY	369 CVNETEQ-----RLGTTGGLY---RISGCDR--TVKELKEK-FLRV 403

Db 881 TYNELKOIYKCKTNNPICKWTNDMNRHFSKEDIYAAKKHMKKCSSLPAIREMOIKITMRY 940
Qy 404 KTVPLL-----SKVDPDTHAISSLKOPTLNRNKEPLTFRFLRAFMMAETDEDN 453
Db 941 HLTTPVRAITIKKGNNISKVDDTHAISSLKOPTLNRKEPLTFRFLRAFMMAETDEDN 1000
Qy 454 SIAMTOAVGELPQANRDTLAFMLIHQRVAQSPHTKMDVANLAKUFGPTVAHAVPNPD 513
Db 1001 SIAMTOAVGELPQANRDTLUFMLIHQRVAQSPHTKMDVANLAEVFGSTIVAHAVPNPE 1060
Qy 514 PVTMSQDIKROPKVVERLLSIPLEYW 539
Db 1061 PVTMLQDIKCKQPKVVERLPSIPLEYW 1086

Search completed: February 1, 2005, 14:15:32
Job time : 169 secs

C;Genetics: A;Gene: FlyBase:rn A;Cross-references: FlyBase:FBgn003263

Query Match 14.7%; Score 477; DB 2; Length 384; Best Local Similarity 40.7%; Pred. No. 8 9e-23; Matches 110; Conservative 44; Mismatches 102; Indels 14; Gaps 6;

Qy 279 QSGGG-NHLHDEVSKT-VIKPESCPGKRTRFGKLSKCRDCRVSHPSPCPCDRCPLCI 336 Db 78 QSHSGLRLREHNFKIKSYVYNGNCVHCRKTRPAMASLRCRACPRICHGCCRQLTVCNI 137

Qy 337 P-TLIGTPVKIGGMLADPVSQTPMPSIIVHCVNEIETQRGLTETGLYRISGGCDRTVKE 395 Db 138 PQPQIGTR--RGCLSDYAPRVAWPWPAITVYCITEEARGLQQESLYRVSSTREKCR 193

Qy 396 LKEKFPLRVTVPFLKSKVUDHICSLKUDFLRNLKEPLTFLRNLRAFMEEA81TDEDSI 455 Db 194 LRRKULRGKSTPHLGN-KDTHLCCVQKDFRLQVHP1P1YHRRDFEATRHDRLAVE 252

Qy 456 AAMYQAVGELPQANRDTLAFMLHQLQVQAQSPTKMOVANLAKVFGPTIVVALAVPNPDDP 515 Db 253 MAVTYLAVLIEBLHQHRTDTAYLMLHWQKIAESPAVRMTVNLAVIFAPTLFG-----DLD 306

Qy 516 TWSQDIKKQPKVVERLISLPLEWSQFMM 545 Db 307 LTLLENNVTVWQRLVVKVLLMPAGFWSQFLEV 336

RESULT 5

554307 myosin heavy chain - rat

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C;Accession: S54307 R;Reinhard, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M.

A;Title: A novel type of myosin implicated in signalling by rho family GTPases.

A;Reference number: S54307; MUID:9518874; PMID:782993

A;Accession: S54307 A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA A;Residues: 1-1980 <REI>

A;Cross-references: UNIPROT:Q63358; EMBL:X77609; NID:9639998; PIDN:CAA54700.1; PID:96399

C;Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C z1

C;Keywords: nucleotide binding; P-loop

F:149-942/domain: myosin motor domain homology <MMOT>

F:149-246/Region: nucleotide-binding motif A (P-loop)

F:1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 10.7%; Score 348; DB 2; Length 1980; Best Local Similarity 22.1%; Pred. No. 1.Je-13; Matches 160; Conservative 105; Mismatches 262; Indels 196; Gaps 25;

RESULT 6

559256 myosin-IXb [similarity] - human

C;Species: *Homo sapiens* (man)

C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C;Accession: A59256; 161700 R;Wirth, J.A.; Jensen, K.A.; Post, P.L.; Bement, W.M.; Mooseker, M.S.

J. Cell Sci. 109, 653-661, 1995

A;Title: Human myosin-IXb, an unconventional myosin with a chimerin-like rho/rac GTPase

A;Reference number: A59256; MUID:97063843; PMID:8907710

A;Accession: A59256 A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA A;Residues: 1-2002 <NTR>

A;Cross-references: UNIPROT:Q14788; GB:042391; NID:9114772; PIDN:AC50402.1; PID:9147.

R;Bement, W.M.; Hasson, T.; With, J.A.; Cheney, R.E.; Mooseker, M.S.

Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994

A;Title: Identification and overlapping expression of multiple unconventional myosin genes

A;Reference number: A55758; MUID:9429418; PMID:8022818

A;Accession: 161700 A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA A;Residues: 1-2002 <RES>

A;Cross-references: GB:L29149; NID:9457257; PIDN:AAA20912.1; PID:9531142 C;Genetics:

A;Gene: GDB:MYOB; OMIM:602129 A;Map Position: 19p13.1

C;Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C z1

F:149-941/domain: myosin motor domain homology #status atypical <MMO>

F:239-246/Region: nucleotide-binding motif A (P-loop)

RESULT 7

1404 LSPGSQVDSKSTPKRLFLHKT-----KKSLEGABELENASVGHVLEATMKKOLEA 1458

Query Match 10.3%; Score 334; DB 2; Length 2022; Best Local Similarity 23.0%; Pred. No. 1e-12; Matches 147; Conservative 111; Mismatches 266; Indels 116; Gaps 26;

Db 1450 GQTVSEKMRSEVKITNAEIKFLDFPLNKVNDLRSQKTIESTIEATERFRSNIK 1509

Qy 22 LSPGNEVO-----PTOLAKDFEDPRKKWQ---RTDHLCYKDLIMKATTERSALDV 70

Db 1510 TMSVPGNGKIHVGKDLMENYQTVWSNLAAERGEKDNLVLFNQFSLDFFIRSYNKT-D 1568

QY	259	SIUNRSRQEKPRTEDUSVGIPUSNNGKLUHDKVTKAPESCPVCEKKGALUS--LRC	316
Db	66	ATJKNEOLPKB-----KVHNFKVHTRGPHCEYCA-NFMWGLIAGQVKC	111
QY	317	RDPVVSHPRECRCPLCPICPTILGTVKICRGMLADFSVOSTSPMTSPSTIVVHCVBIEQR	376
Db	112	ADGQLNVKHQCSQAVPNCKPDLKHVK-KVSCDLITLVKAHITKRPVMVDMCIRIESR	170
QY	377	GRETGLURISGCDRTKELKEKFRL--VKTVPLLSKVDDTHAICSLKDKPLNKEPL	434
Db	171	GLNSEGLYRVSGLDIEDVKAFDRIDGEKADISVNNYEDINITGALKYFRDPLIPLI	230
QY	435	TFKLARAMEAETIDNSIAAMYQANGELBQANETDLMHJORVQSPHTK--M	491
Db	231	TYWAPYKTESAKIVDPEOELTBLHEALRSLPPAHCBTLYIMAHLKRV--TLHEKENLM	288
QY	492	DVANLAKYFGPTIVAHAVPNPDPFTVMSQDIPKQPKVVERL	532
Db	289	SPN1GTCGCP1MPS--PPTMLAINDTYPVPLIPLI	327

A; Reference number: A43953; MUID:92252621; PMID:1374499
 A; Accession: A43953
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-299 <GEO>
 A; Cross-references: HVC-associated telencephalon
 A; Note: sequence extracted from NCBI backbone (NCBN: 98891, NCBI_P: 98892)
 F:46-95/ Domain: protein kinase C zinc-binding repeat homology <KZ2>

 Query Match 9.9%; Score 320; DB 2; Length 299;
 Best Local Similarity 31.6%; Pred. No. 5.3e-13;
 Matches 92; Conservative 47; Mismatches 106; Indels 46; Gaps 10;
 QY 259 STLNRSQLEPRTMTDSVTPQSNGMRLHD**F**USKVTKPESCVPGKRIKGKLS-LKC 316
 Db 31 ATLKENERHVPKYE-----KVNFKVHTFRGPHWCYCA-NFMWGLIAGQVRC 76
 QY 317 ROCRVSHSPCERDRCPCTP**L**-----IGTPKIGEMLADTVQSQPMISIV 366
 Db 77 ADCCGLNVTKQCSQVNPDCPKD**L**KVVKVVSQDITLTK-----AHFTKR----PNAV 125
 QY 367 VHCNEFEBQRGLTETGLYRISGCDRTVKEKEKFLR--VKTFLLSKVDIHAICSLKD 424
 Db 126 DMCIREIELESRGUNSEGURVSGSDLIDVDRMAFDRDGEKAIDSVNMYEDINITGAIKL 185
 QY 425 FLRNKLEPLTFLRNRAFMEAAITDEDNISTAMYQAVGELPQANRDTLAFLMHORVA 484
 Db 186 YFRDLPLIPLITYDAYPKFIESAKITDPPDQELETIHEALKLPPAHCTLYRQMLKRV- 244
 QY 485 QSPHTK--MDVANLAKVFGPTVAHAVNPDPVTMSDICKRQPKVVERL 532
 Db 245 -TUEKENLMSAENLGTVFQPTLM--RAPELDAALNDIYRQVLVEMLI 292

RESULT 10
 T39954
 probable grpase activating protein homolog - fission yeast (Schizosaccharomyces pombe)
 C; Species: Schizosaccharomyces pombe
 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C; Accession: T39954
 R; Xiang, Z.; Aves, S.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, January 1999
 A; Reference number: 221893
 A; Accession: T39954
 A; Status: preliminary; translated from GB/EMBL/DBDJ
 A; Molecule type: DNA
 A; Residues: 1-695 <XIA>
 A; Cross-references: UNIPROT:O94466; EMBL:AL035065; PIDN:CAA22624.1; GSPDB:GN00067; SPDB:
 A; Experimental source: strain 972h-; cosmid C23G7
 C; Genetics:
 A; Gene: SPBc23G7_08C
 A; Map position: 2

 Query Match 9.9%; Score 308; DB 2; Length 695;
 Best Local Similarity 23.7%; Pred. No. 1e-11; Matches 137; Conservative 87; Mismatches 223; Indels 132; Gaps 23;

 QY 35 K0PDEFRKKWQRTDHE---LGKVKDLIMKAEF-**R**SAIDVKLKHARNQDV**E**IK--RR 86
 Db 145 KSTKEYAKQKQENAYLEAMQMD**S**KSRSRKGAEEYRNALDK----NTGDSQXKV**E**FK 199
 QY 87 QRAEADCEK**E**LERQ**I**Q**L**IREBMLMD**T**SGSIOL**S**RS-**R**KS**A**LF-----LNRGOPS 134
 Db 200 PPKSNALQ**T**KEDEARL**K**AE**N**AE**S**DM**H**SK**E**TA**N**Q**V**OK**L**CI**H**R**P**NY**I**K**Q**FF**S**LO**R**E**T**ES 259
 QY 135 S**S**VAGN**G**KL**S**T**B**SG**S**LS**I**DI-----SF**K**Y**D**E**S**LO**W**D**S**SL**S**U**V**TF**K**IK 178
 Db 260 S**L**TAN**Y**LR**Y**TK**L**C**E**ST**N**TL**I**NG**G**LT**R**PK**Q**PT**P**TM**C**GL**O**LR**D**NT**N**ANT**D**P**V**Q**V**U**H**A-S**I**K 318
 QY 179 K**R**E**K**R**E****R**-----S**R**Q**V**D**G**P**G**P**V**K**K**T**R**S**G**S**A**D**G**N**E**S**I**V**A**K**T**V**V**N**D**GG**E**---A 232
 Db 319 H**E**D**N**K**N**P**T**D**A**S**K**U**K**I**Q**P**S**Y**G**S**A**G**K**T**N**P**V**N**P**T-----K**V**T**A**I**P**S---PLQNTNPA 373

RESULT 11
 E59430 PPIPL1-associated RhoGAP protein 1 [imported] - human
 C; Species: Homo sapiens (man)
 C; Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
 C; Accession: E59430
 R; Saras, J.; Franzen, P.; Aspenstrom, P.; Heiman, U.; Gomez, L.J.; Heidin, C.-H.
 submitted to GenBank, December 1997
 A; Description: Homo sapiens PPIPL1-associated RhoGAP 1 (PARG1), mRNA.
 A; Reference number: E59430
 A; Accession: E59430
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-1251 <SAR>
 A; Cross-references: UNIPROT:O15463; GB:NP_004806; PID:94758892; PIDN:NP_004806.1

 Query Match 9.3%; Score 301; DB 2; Length 1261;
 Best Local Similarity 22.4%; Pred. No. 6.4e-11; Matches 153; Conservative 249; Mismatches 249; Indels 160; Gaps 33;
 Matches 153;
 QY 9 RNLFEQLVVRVETLSEGNEVQ**T**QL**A**D**E**DRKK**W**RTD**H**E-LGKVKDLIMKAE**R**SA 67
 Db 372 RRL**E**E**A**Q**V**K-----E**A**DL**E**Y**K**-CV**T**N**V**E**E**R**N**D**V**N**E**T**N**K**T**E**L**A**Q****R**T**L**V**Q**C**D**L**T**L**K**A 427
 QY 68 L**D**Y**V**L**K**H**A**R**N**Q**V**E**D**E**V**E**I**K**R**R**Q**A**B**D**C**K**L**E**R**Q**I**O**L**I**Q**H**E**M**L****D**T**G**S**T**I**S**L**O****S****R****Q****K**-**SA** 124
 Db 428 V**T**N**L**F**M**H**Q**L**Q**A**S**L**A**D**R**L**Q**S**L**C**G**S**A**K**L**D**P****C**Q**E****T**S**E****F**V**K**A**T**N-----T**B**E**K**V**G**N 482

 QY 125 L**A**F**I**N**R**G**O**P**S**S**N**A**G**N**R**L**S**T-----D**S**G**S**I**S**D**I**S**D**K**T**D**S**L**D****W****S****L**V**U****K**T**F**K**R**E 181
 Db 483 N**K**H**L**N**S****Q****P****G****S****F****G****P****A**N**S****L****E****D****V****R****L****P****D****S****N****K****I****B****D****R****C****S****N****S****A****D****I****T**---G**F**S**F****R****S****F****M****S** 539

 QY 182 K**R**R**T**S**R****O**F**V**D**G**P**G**P**V**K**T**R**S****G**S**A**D**G**N**E**S**I**V**A**K**T**V**V**N**D**GG**E**---A 241
 Db 540 D**S****S****E****T**-----G**G**S**E****S****R****S****I****D**-----E**S****I**-----S**P****G**----- 562

 QY 242 W**T**R**S**R**R****K****I****G**T**L**Q**W**N**S****T****I****N****S****H****O****L****E****R****P****R****E****T**-----D**S**V**G****T****Q****S**---N**G****A****R****L****H****D****V****S****K****T****V****K** 296
 Db 563 F**R****K****L****P****R****I****P****S****G****I****M****S****A****D****D****L****E****R****P****S****P****E****T****G****P****N****S****L****T****G****F****K****T****I****M****S****K****A****L****T****K****E****R****L****R****S** 620

 QY 297 P**E**S**C****V****P****C****K****I****R****K****S****I****S****K****C****R****C****R****V****A****H****P****E****C****D****R****C****P****C**-----I**P**-----T**L****G****C****P****V****K****G** 349
 Db 621 P**T****K****C****R****D****C****G****I****V****F**-----Q**G****V****E****C****E****T****L****V****A****H****R****K****C****L****N****V****I****C****G****H****O****K****I****P****G****K****I****H****F**----- 670

 QY 350 M**L****A****D****F**-----V**S****Q****T****S****P****M****I****S****BIV**H****C****N****E****E****BQ**R****G****T****E****G****R****I****S****C****D****R****T****K****E****K****L****R****K****T****V** 406
 Db 671 --A**E****F****T****V****A****K****E****P****D****G****I****P****L****K****I****C****A****S****E****T****E****N****R****A****L****C****G****O****Y****I****R****V****C****G**-----N**K****I****K****E** 716****

Db 271 LTLHDNRYQKULIVQ-
QY 407 PILSKVDD---DI-----HATCSLLKDFRLNLUKEPLTFLRNLRAFMEA---ITDE 451
Db 717 KCLLALENGNMHLVDISERSSHPIDCVDVLYLRLQPERPLFILRLYKEFDLAKERIQHNEE 776
QY 452 DNS-----IAAMYQAVGELPQANRDTLAFMLIHLQRYA-QSHTK 490
Db 777 QEVKVKNSLEDKRPNCIEINRILKSKDLRQPLASNFNSLHFLVHLKRVDHAEENK 836
QY 491 MDVANLAKVFGPHTIVAHAVPNPD--PVMSQ- DIKQPKVVERLISLPLEWYSQFM--- 543
Db 837 MNSKNLGIVFGEPLR--PPTQATPITISLAEYSNQARLVEFLIT---YSQKIFDG 888
QY 544 -MVEQENIDPLAVIENS---NRFSTPQTPDPIKVLQSLIGAPVTBHQQLKTPSSLSQVR 599
Db 889 SIQPOQDMCSIGVVDQGCFPPKPLISPEERDIERSMKSLUFFSSKEDIHTSESKIFERAT 948
QY 600 STILTKNTPRPGSKSKSATNLGR 621
Db 949 S-----FEESERKQNALGK 962

RESULT 12

S29956 N:Alternate names: GTPase-activating protein
C:Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
R;Leung, T.; How, B.E.; Manser, E.; Lim, L.
J. Biol. Chem. 268, 3813-3816, 1993
A;Title: Germ cell beta-chimaerin, a new GTPase-activating protein for p21rac, is specific for the E24-91 domain: protein kinase C zinc-binding repeat homology <K22>
A;Reference number: A45485; MUID:93179371; PMID:8440677
A;Accession: A45485
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-295 <LEU>
A;Cross-references: UNIPROT:Q03070; EMBL:X69489; NID:957526; PIDN:CAA49244_1; PID:957527
A;Experimental source: testis
A;Note: sequence extracted from NCBIP:125731
R;Leung, T.; How, B.E.; Manser, E.; Lim, L.
submitted to the EMBL Data Library, November 1992
A;Description: Germ cell beta-chimaerin, a new GTPase-activating protein for p21rac, is
A;Reference number: S31398
A;Accession: S31398
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-295 <LEU>
A;Cross-references: EMBL:X69462; NID:955816; PID:955817
A;E24-91/Domain: protein kinase C zinc-binding repeat homology <K22>

Query Match 9.1%; Score 294; DB 2; length 443;
Best Local Similarity 29.3%; Pred. No. 4.1e-11; M:Matches 11; Indels 32; Gaps 8;
Matches 81; Conservative 52; M:Matches 11; Indels 32; Gaps 8;

Db 285 RLHDVFVSKTVIKPESCPGKGKIKRGKLS--LKCRCRDRVSHPREGDRCPICPILTG 342
Qy 188 KTHNPKVHTFRGPWHCEYCA-NFMWGLIAGQEVRCSDGLNVHKQCSKHPNDQCDPKR 246
Qy 343 PVKIGEGLMADFSQTSQSPMIPSIVHCVNEIEQRGITETGIRISQCDRTVKELKEKFLR 402
Db 247 K-KVYCCDLTIVKAINTQRMVWDICIRELEARGKSEGIVRSCETEIEIDVMAFDR 305
Qy 403 VKTVPPLSKVQ-----DIHACLSLKDFLRNKPLPFLRNRAFMEAETIDBNSI 455
Db 306 DG-----EKADISANIPDINITGALKLYFRDLPIPIITDYSKEFEAKKISNAEERL 360
Qy 456 AMYQAVGELPQANRDTLAFMLIHLQRYAQSHTK-MDVANLAKVFGPTIVAHAVPNPD 514
Db 361 EAHEVIMLPPAHYETVRLMTHLKRVTMNEKDNMNAENLGVFGPTM--RPEDST 418
Qy 515 VTMQDQIKRQPKVERLISLPLEWYSQFMVQEONI 550
Db 419 LTLHDNRYQKULIVQ-
QY 425 RLUHDVFVSKTVIKPESCPGKGKIKRGKLS--LKCRCRDRVSHPREGDRCPICPILTG 342
Db 40 KTHNPKVHTFRGPWHCEYCA-NFMWGLIAGQEVRCSDGLNVHKQCSKHPNDQCDPKR 98
Qy 343 PVKIGEGLMADFSQTSQSPMIPSIVHCVNEIEQRGITETGIRISQCDRTVKELKEKFLR 402
Db 99 K-KVYCCDLTIVKAINTQRMVWDICIRELEARGKSEGIVRSCETEIEIDVMAFDR 157
Qy 403 VKTVPPLSKVQ-----DIHACLSLKDFLRNKPLPFLRNRAFMEAETIDBNSI 455
Db 158 DG-----EKADISANIPDINITGALKLYFRDLPIPIITDYSKEFEAKKISNAEERL 212
Qy 456 AMYQAVGELPQANRDTLAFMLIHLQRYAQSHTK-MDVANLAKVFGPTIVAHAVPNPD 514
Db 213 EAHEVIMLPPAHYETVRLMTHLKRVTMNEKDNMNAENLGVFGPTM--RPEDST 270
Qy 515 VTMQDQIKRQPKVERLISLPLEWYSQFMVQEONI 550

RESULT 14

A53764 N:Alternate names: GTPase-activating protein
C:Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
R;Leung, T.; How, B.E.; Manser, E.; Lim, L.
J. Biol. Chem. 269, 12888-12892, 1994
A;Title: Cerebellar beta-chimaerin, a GTPase-activating protein for p21 Ras-related Rac
A;Reference number: A53764; MUID:94230370; PMID:8175705
A;Accession: A53764
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-466 <LEU>
A;Cross-references: UNIPROT:P52757; GB:L29126; NID:9457229; PIDN:AAA19191_1; PID:9457230
F;157-137/Domain: SH2 homology <SH2>
F;213-262/Domain: protein kinase C zinc-binding repeat homology <K22>
Query Match 9.1%; Score 293.5; DB 2; Length 466;
Best Local Similarity 25.7%; Pred. No. 4.7e-11; M:Matches 15; Indels 63; Gaps 12;
Matches 98; Conservative 66; Mismatches 15; Indels 63; Gaps 12;

Db 199 KCTRSIGSAVQGNESIVAKTIVTVDGGPTEAVSTIETV-----YWRSSRKTGTL 252
Qy 119 KCTRSIGSAVQGNESIVAKTIVTVDGGPTEAVSTIETV-----YWRSSRKTGTL 252
Db 116 KRFESTIDLVTDGLITIYIETKA-----EYISMNTNPYHIGYIILRKV-- 164

QY 253 QPNNSDSTNSRQLEPR-----TEPDVCTPQNSGM-----RHDFVSKT 293
 Db 165 -----SRLRSRSKNEPRKTNVTBHTAVEKUSSLVRAALTHNDHNHYKTHNFKVHT 219
 QY 294 VIKRBCSPCGKIKPGULS-LKCRDRVVISPBPCRDRCPCLCPICTIGTPKIGEML 351
 Db 220 FRGPHWCEYCA-NFMWGLJATQYTRCSDCGQNLNVHQCSKHVPPDCQDPLKRIK-KVYCCDL 277
 QY 352 ADFSQTSQPMPSIVHCVNEIRQRLTETGLYRISGCDRTVKEKFLKFLR-VKTVPL 409
 Db 278 TTUVKAHQTORPMVWDICIREBARGLUSKSEGGLRVSGFTBHEDVKMAFRDGEKADISA 337
 QY 410 SKYDHDIAICSLKDFLNLKELULTRFLNRAMEAETIDENSIAAMYQAVGELQAN 469
 Db 338 NVVPDINITITGALKLYFRLPPIVTDYTKSFDAAKSLNADERLEAVHEVILMLPPA 397
 QY 470 RDTLAFMLHQLQVAQSHTK-MDVANLAKVFGPTIVAHANVPPDPVTMSQDKRQPKWV 528
 QY 398 YETLRYLMILHQLKWTMNEKDNFMAENLGIVGFTLM-RPPEDSTLTLHDNRYQKLIV 455
 QY 529 ERLLSLPLEYWSOPMMVQBNI 550
 Db 456 Q-----ILINEDV 464

RESULT 15

QY 310 GKLSL-----KCRDCR-WUSHPECD--RCPLPQIPTL----- 340
 Db 483 GKWTLSSAQTHOLRRLRGPAKCRECAFMSGTECECFLTCRKRCLETLLCGRRL 542
 QY 341 -GTPVKIGEML--ADFSQTSQPMPSIVHCVNEIRQRLTETGLYRISGCDRTVKE 395
 Db 543 PARTPL-FGVDFLQLPDPPEE---VPFWVTKTABIEHRAFDVQIYRVSGRVVER 597
 QY 396 LKKEFLRVTVPPLSKDHDIAICSLKDFLNLKELULTRFLNRAMEAETIDED-- 452
 Db 598 LCOAFENGALVBLSG-NSPHDVSSVJKRFQELTEVIFPFLYDATISLAKTHAPGD 656
 QY 453 -----NSTAMYQAVGELPQANDTFLATLHMQV-AQSPHTRKNDVANLAKYFGP 502
 Db 657 DRGTPSSPDPDVRSKLTULVOLPDSNTNTRLHLV AHLFRAARFMENKMSANLNGIVFGP 716
 QY 503 TIVAHAVNPD-----PVTMSQDKRQPKVVERLILSLPLEYWSOPMMVQENIDPLH 554
 QY 717 TLLR---PPDGPRAAARIPVCLLSDGHQAOLVE-----FLIVHYEQIFGMD 760
 QY 555 VIENSAFSTPQTDIKVSLLGPVTT-----PEHQ---LLKTPS-----SSASLQ 596
 Db 761 ELFQ---ATEPPQDPSAPAPLITCSQPPPHLDSDQPPVTLASPGPDPQHHSLEQ 816
 QY 597 RYRSTLTK-NTRFGSISKSATN-----LGRQ---GNNFASP 629
 Db 817 HPTATPMSIPTPOSQDRBVAEDTKDGGEVSSQGPBDSSLGTSQRHFSRQP 869

Query Match 9.0%; Score 291; DB 2; Length 970;
 Best Local Similarity 22.6%; Pred. No. 1.9e-10;
 Matches 188; Conservatve 112; Mismatches 273; Indels 260; Gaps 40;
 C;Species: Homo sapiens (man)
 C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
 C;Accession: D59435
 R;Areta, S.; Berger, P.; Berger, R.; de Gunzburg, J.
 Submitted to GenBank, November 2000
 A;Description: GMIP, a Gem interacting protein.
 A;Reference number: D59435
 A;Accession: D59435
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-970 <ARE>
 A;Cross-references: UNIPROT:Q9P107; GB:NP_057657; PID:97706107; PIDN:NP_057657.1

Query Match 9.0%; Score 291; DB 2; Length 970;
 Best Local Similarity 22.6%; Pred. No. 1.9e-10;
 Matches 188; Conservatve 112; Mismatches 273; Indels 260; Gaps 40;
 QY 13 EQLVRVILTSBENEVQFIQLOAKDFEDERKK--W-ORTDHSLGKYKDLMLKETRSA 67
 Db 81 BEEDLRL-IRTKGEVDAALEYAKTWSRVAKELLAWTEKRAKSYLEFAKSTMKTAEGAKV 139
 QY 69 LDVK-----LKH-----ARNQDVDE 82
 Db 140 IQQOSHMPQIYITLFLHDLDSLGLTAMETVAQOKRDYIOPLAKRTEIEKWRKKEKOW 199
 QY 83 IKRQRQAEDCEKLER-QIQLR--EMMCDTSQSIOLSEBQKSLAFLNRGOPSSNAG 139
 Db 200 MKQOKRMNEAVQQLRQLOQYVQRSEDIRARSQSPEDSAPQAS-----PGPSQO 250
 QY 140 NKRUSTTDESGLSLSDPSFKTDESLDWSSLVTKFKKRE---KRRSTS--ROFY-D 192
 Db 251 ERRRSREBAAQ-----KAQEAALYQACREANARQDIEIAKORIVSVRKLVFQ 302
 QY 193 GPPGPVKKTRSI---GSAVDQGENESTIVAKTIVPNDG-----PIE 231
 Db 303 GDEVRILRVITSLFGLRGAQAEGRPRAFAAECAPFBFGQRVOEFVRLRPEAPPPPP 362
 QY 232 AVSTIETPWHTS-----RKIGTQ-----PWNST-----LNSRQLEPRT 271
 Db 363 AFSPQEFPLPSLNSPDLTRKLGKUSPGLPPLRDENSAPGPWEDPGTGMWQGPCTG 422
 QY 272 TDSVG-----TPOSGNGMRLHDFVSKTVIKPES-----VRCGKRTKF 309
 Db 423 VDSVGGSSRSLSDPSSPAGTQLYKASSCTESSDDFEERDPDLDGLGNGLGSPP 482

Search completed: February 1, 2005, 14:20:01
 Job time : 57 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 1, 2005, 14:09:12 ; Search time 40 seconds

Perfect score: US-09-881-736A-2

Sequence: 1 MDTMLMLNVLNLFQEVRRV. SKSASNLGROQNRFASPMLK 632

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 1%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: * /iaaa/5A_COMB.pep: *

1: /cgn2_6/podata/1/iaaa/5B_COMB.pep: *

2: /cgn2_6/podata/1/iaaa/6A_COMB.pep: *

3: /cgn2_6/podata/1/iaaa/6B_COMB.pep: *

4: /cgn2_6/podata/1/iaaa/PCUS_COMB.pep: *

5: /cgn2_6/podata/1/iaaa/backFiles1.pep: *

6: /cgn2_6/podata/1/iaaa/backFiles1.pep: *

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	301	9.3	1261	3 US-09-080-855-2
2	301	9.3	1261	4 US-09-080-855-2
3	270.5	8.3	2548	3 US-09-172-422-1
4	257.5	7.9	165	5 PCT-US93-03076-10
5	230	7.1	140	6 PCT-US93-03076-9
6	214.5	6.6	547	4 US-09-855-323-15
7	210	6.5	1513	5 PCT-US93-03076-5
8	202.5	6.2	946	4 US-09-539-092-1230
9	200.5	6.2	1702	4 US-09-854-133-434
10	198.5	6.1	645	4 US-10-164-595-40
11	197.5	6.1	639	4 US-10-164-595-73
12	195.5	6.0	537	4 US-09-270-767-32573
13	195.5	6.0	537	4 US-09-270-767-47790
14	192	5.9	333	4 US-09-507-765-32
15	192	5.9	433	4 US-09-507-765-30
16	191	5.9	433	4 US-09-507-765-31
17	191	5.9	2071	3 US-09-155-522-6
18	188.5	5.8	439	4 US-09-507-765-33
19	186	5.7	169	4 US-09-248-796-14549
20	183.5	5.7	162	5 PCT-US93-0376-8
21	179.5	5.5	581	4 US-09-270-767-33206
22	179.5	5.5	581	4 US-09-270-767-48423
23	172	5.3	362	4 US-09-270-767-41652
24	169.5	5.2	1007	4 US-09-538-092-736
25	161	5.0	1013	3 US-09-415-522-8
26	151	4.7	282	4 US-09-248-796-20596
27	150.5	4.6	197	4 US-09-270-767-33381

RESULT 1

US-09-080-855-2

SEQUENCE 2, Application US/09080855A

Patent No. 6083721

GENERAL INFORMATION:

APPLICANT: Staras, Jan

APPLICANT: Aspenström, Pontus

APPLICANT: Hellman, Ulf

APPLICANT: Gómez, Leonor Jorge

APPLICANT: Helin, Carl-Henrik

TITLE OF INVENTION: PAR, A GRIPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL

CURRENT APPLICATION NUMBER: US/09/080, 855A

CURRENT FILING DATE: 1998-05-18

EARLIER APPLICATION NUMBER: 08/805, 583

EARLIER FILING DATE: 1997-02-25

NUMBER OF SEQ ID NOS: 39

SOFTWARE: fastSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 1261

TYPE: PRT

ORGANISM: Homo sapiens

Query Match 9.3%; Score 301; DB 3; Length 1261; Best Local Similarity 22.4%; Pred. No. 7.9e-19; Matches 153, Conservative 120; Mismatches 249; Indels 160; Gaps 33; Query 9 RNLFBOLVVERVEILSEGNTVQFIQLAKDFEDFRICKWQRTDHE-LGKYKDLIMKABTERSA 67 Db 372 RLBBEALKEV--EADELYKV-CVTVNFEERRDVNTKREILQLRITVFOCDLTKA 427 Qy 68 LDVKUKHARNQDVTEIKRKRRAEADCEKLERQIQLIREMMCDTSQSIQLEEK--SA 124 Db 428 VTNULFHMGHQLQASLADLQDLSQGSAKLYDPSGSEYSEFVKATNS----TEEEVKDGNV 482 Qy 125 LAFJNLRGQDSSSNAGNKRISTI--DEGSISLSDISFDKTDIDESLDWDSSLKVTKLKKRE 181 Db 483 NKHJNQSSQFSGFGPANSLSADVVRUPDSSNKEEDRCNSNADIT--GPSPIRSTPGMFS 539 Qy 182 KRSTTSRQFVDPGPVVKURTSQGAVDGNESIVAKTFTVTPVNDGPRTEAVSTIETVY 241 Db 540 DSEST-----GGSSRSRSLDS-----EST-----SPGD----- 562 Qy 242 WTRSRKIGTLQPMNSDSTLNROLEPRTET--DSVGPQSQ--NGGMLHDVFSKTVK 296 Db 563 FHRKLPRTSSGTMSSADDLEREPSPSETGPMUSLGPTRKTMKSAALTHKF--RKLAS 620 Qy 297 PESCVPGKRIKFKGKLSLXKCRDCRVSHRECCRDRCLPLC---IP---TIGTPVKIGE 349

ALIGNMENTS

RESULT 2

US-09-566-076-2

; Sequence 2, Application US/09566076

; Patent No. 647575

GENERAL INFORMATION:

; APPLICANT: Saras, Jan

; APPLICANT: Aspenstrm, Pontus

; APPLICANT: Hellman, Ulf

; APPLICANT: Heldin, Carl-Henrik

; TITLE OF INVENTION: PARC, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PPML

; FILE REFERENCE: I0461/7030

; CURRENT APPLICATION NUMBER: US/09/566,076

; CURRENT FILING DATE: 1998-05-18

; EARLIER APPLICATION NUMBER: 09/080,855

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 1261

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-566-076-2

Query Match 9.3%; Score 301; DB 4; Length 1261;

Best Local Similarity 22.4%; Pred. No. 7.9e-19; Indels 160; Gaps 33;

Matches 153; Conservative 249; Indels 160; Gaps 33;

Qy 9 RILFEQQLVRRVAILSEGNEWQFIQLAKDFEDRKKWQRTDIE-LGKVQDLMAERTSA 67

Db 372 RKELEEAQKVE--EADELKVY-CVNVVERNDVENTKRLAQIRTLFOCDITKA 427

Qy 68 LIVVKLKHARNQYDVEKRRQARABDCEKLERQIOLIREMMLMDTSSQIOLSEBOK--SA 124

Db 428 WTVNLFLHMQHLQMASLADLQSLCAGKUDPGQEVSEFVKATNS---FEEKVDGKV 482

Qy 125 LAFLNGCOPSSNAGNRLSTI--DEGSISLSDISDKTBSLDWDSLWVJKTFLKKE 181

Db 483 NKLHNSSQPSGFPANSLEDVVRLPDSNSNKTEBEDCSNSADIT--GPFSEFIRSWTGMFS 539

Qy 182 KKRSTSRQFDGPPGPVKTRSIGSAVDQGHNISIVAKTVTVFNDGGPIEAVSTIETVPY 241

Db 540 DSEST-----GSSSESLDS-----ESI-----SPGD----- 562

Qy 242 WTRSRRTGTQWPNSDTSNRSQERPTER--DAGVTROS--NGGMRJADPFSKTVK 296

Db 563 FHRKLPRTPSSGTMSSADDLDREREPPSSETPGNSLGTFFKLMKALTHKF--RKLRS 620

Qy 297 PBCVPGKRRKGKULSKCDRCVSHPSGCRDRPLC--IP--TUGTPVKIGG 349

Db 671 --AEFTLVAKKEPDGIFFLIKICASELENRACILOGYRG--NKKTE 716

Qy 407 PLISKVD----DI----HAICSLKLDFRLNKEPLTRPLNRAFMEA--ITDE 451

Db 717 KCLALENGMLHLDISFRSSHDCIDCVLKLVYRQLPEPFILRFLYKEFDLAKIEQHNEE 776

Qy 452 DNS-----IAWYQAVGELPOANRDTAFLMILHQVRA-QSPHTK 490

Db 777 QPTKKNSLEDKWPNCIETINRILLKSLDRLQLPASNFNSLHFLVHLKRVDHAEENK 836

Qy 491 MDVANLAKVFGPTIVAHAVPND--PVTM50--DICKRQPKVERLISLPLEYWSQFM-- 543

Db 889 SLQPODVMCSIGVNDQCCFPKPLSPEERDIERSMKSLFFSSKEDIHTSESESKFERAT 948

Qy 600 STLKVNPRFGSKSKSATNLR 621

Db 949 S-----FEESERKONALGK 962

Qy 242 WTRSRRTGTQWPNSDTSNRSQERPTER--DAGVTROS--NGGMRJADPFSKTVK 296

Db 563 FHRKLPRTPSSGTMSSADDLDREREPPSSETPGNSLGTFFKLMKALTHKF--RKLRS 620

Qy 297 PBCVPGKRRKGKULSKCDRCVSHPSGCRDRPLC--IP--TUGTPVKIGG 349

Db 671 --AEFTLVAKKEPDGIFFLIKICASELENRACILOGYRG--NKKTE 716

Qy 407 PLISKVD----DI----HAICSLKLDFRLNKEPLTRPLNRAFMEA--ITDE 451

Db 717 KCLALENGMLHLDISFRSSHDCIDCVLKLVYRQLPEPFILRFLYKEFDLAKIEQHNEE 776

Qy 452 DNS-----IAWYQAVGELPOANRDTAFLMILHQVRA-QSPHTK 490

Db 777 QPTKKNSLEDKWPNCIETINRILLKSLDRLQLPASNFNSLHFLVHLKRVDHAEENK 836

Qy 491 MDVANLAKVFGPTIVAHAVPND--PVTM50--DICKRQPKVERLISLPLEYWSQFM-- 543

Db 889 SLQPODVMCSIGVNDQCCFPKPLSPEERDIERSMKSLFFSSKEDIHTSESESKFERAT 948

Qy 544 -MVEQENIDPAPVTE--NAFSTQTPDKVSLIGPVTPEHQQLKTPSSSLSQVR 599

Db 889 SLQPODVMCSIGVNDQCCFPKPLSPEERDIERSMKSLFFSSKEDIHTSESESKFERAT 948

Qy 600 STLKVNPRFGSKSKSATNLR 621

Db 949 S-----FEESERKONALGK 962

RESULT 3

US-09-172-422-1

; Sequence 1, Application US/09172422A

; Patent No. 630485

GENERAL INFORMATION:

; APPLICANT: Adams, Arwen E.

; APPLICANT: Chiu, Choi Ying

; APPLICANT: Duhl, David

; APPLICANT: German, Susan W.

; APPLICANT: Leng, Song

; APPLICANT: Sheffield, Val

; APPLICANT: Welch, Juliet

; TITLE OF INVENTION: MYOSIN IIA AND CYCLIC NUCLEOTIDE GATED POLYNUCLEOTIDES, POLYPEPTIDES, TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF

; FILE REFERENCE: 200130-442

; CURRENT APPLICATION NUMBER: US/09/172,422A

; CURRENT FILING DATE: 1998-10-14

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 2548

; TYPE: PRT

; ORGANISM: Homo sapien

; US-09-172-422-1

Query Match 8.3%; Score 270.5; DB 3; Length 2548;

Best Local Similarity 24.4%; Pred. No. 2e-15; Indels 125; Gaps 24;

Matches 130; Conservative 203; Indels 125; Gaps 24;

Qy 143 LSTIDEGSISLSDISDKTBSLDWDSLWVJKTFLKKE 180

Db 1864 LKSMDE--FLJKVN-DLDNEBSDKADLTVDFVKAKKEFRQN-----IFSFY 1908

Qy 203 SIGSAVTDQGN-----ESIVAKTVTVFNDGGPIEAVSTIETVPYR 247

Db 1909 SSALAMDDGKSIRYKDLYALFQEOLKTRMLERODSLSGESPVRVWVNTFKVFLDBYNEF 1968

Qy 248 KTGLOPWNSTL---NSRQLPPTEDSUGVPGQSONGMRUHDVFUSKTVKRESCVP 302

Db 1969 KT-----DCATPKVPTKERRQKKEBTDJV--EERNG---HIFKATOISIPTVCEY 2015
 Qy 303 CGKRKIKGKLJLKCRCDCRUVVSHPECRDRCPCLPCIPPTIIGTPVKG-----GMLADFV 355
 Db 2016 CSSLIWIMDRASVCKLCKVACHKK-----CLKTTAKCSKKDPELSSORGVELSRL 2068
 Qy 356 SQTSPMPSIVVHCVNELEORGITETGTYRISGCDRTVKELKEKFLRVKTVPLSKYD-----414
 Db 2069 TSBDRTVPLVKEKLINYEMHGLYTEGIYRKSCSTNKTKELRO---GLDTDAESVNLDY 2125
 Qy 415 -IAICSLKDFLRNLKEPLTFRLNRAFMEEAITBDSNIAAMQAVGELPQANRDTL 473
 Db 2126 NHVITASVFKQWMLRDEMLPMLTFELYEEFLRANGLQERKEETRGVSVQDLSRTHNTL 2185
 Qy 474 AFLIMIHIQVRA-OSPHTKMDVANLAKVFGPTVVAHAVENNPDPVMSQDIKRQPKVVERL 532
 Db 2186 ERLLFLHVLRLQDENTRMSANALAIVFACIL-RCPDTDPLQSVDISKITTCVE-- 2241
 Qy 533 SULPEYLNQSQFMMYEQEN-----IDPLHVIENSNAFSTPQPDIVSL-----575
 Db 2242 -----LIVVEMQNKVKARLKDISLLEFAENK-----AKTRLSSLRRSMGKRI 2284
 Qy 576 -----GPVTTPHQLLKTPSSSLSQRVSTLTKNTPRGSKSATNLGRQ 622
 Db 2285 RRGNYPGB-SPS--VVRLPSVSDVSE--ETUT-----SEAMETDIEQ 2324

RESULT 4 PCT-US93-03076-10

; Sequence 10, Application PC/rus9303076

; GENERAL INFORMATION:

; APPLICANT: Whitehead Institute for Biomedical Research

; TITLE OF INVENTION: GAP-Associated Protein p190 and

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: 2 Militia Drive

; STATE: MA

; COUNTRY: US

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.2.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/03076

; FILING DATE: 19930331

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Granahan, Patricia

; REGISTRATION NUMBER: 32.227

; REFERENCE/DOCKET NUMBER: WH192-03A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-861-6240

; TELEFAX: 617-861-9540

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 140 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US93-03076-9

Query Match 7.1%; Score 230; DB 5; Length 140;
 Best Local Similarity 38.8%; Pred. No. 1.1e-13; Gaps 2;
 Matches 54; Conservative 24; Mismatches 59; Indels 2; Gaps 2;

Qy 369 CVBIEQRLTENGLYRISGCDRTVKELKEKFLRVKTVPLSKYDIAICSLKFLR 427
 Db 1 CVBIEQRLTENGLYRISGCDRTVKELKEKFLRVKTVPLSKYDIAICSLKFLR 60
 Qy 428 NLKEPLTFRLNRAFMEEAITBDSNIAAMQAVGELPQANRDTLAFMLHQLRVAQSP 487
 Db 61 ELPEPLTFDEFYNNFAEGTALSPVAKESCMNLILLSPANLITFFFLDHLKRVKE 120
 Qy 488 H-TKMDVANLAKVFGPTV 505
 Db 121 AVNKNLHNLATVFGPTL 139

RESULT 6 US-09-855-323-15

; Sequence 15, Application US/09855323

; Patent No. 6602667

; GENERAL INFORMATION:

; APPLICANT: Walker, Michael G.

; APPLICANT: Volkmarth, Wayne

Query Match 7.9%; Score 257.5; DB 5; Length 165;
 Best Local Similarity 37.9%; Pred. No. 3.4e-16; Gaps 4;
 Matches 64; Conservative 33; Mismatches 63; Indels 9; Gaps 4;

Qy 369 CVNIEQRLTETGIRISGCDRTVKELKEKFLR-VKTVPLSKYDIAICSLKFLR 426
 Db 1 CIREIESRGLNSEGLEYRVGGFSDLIEDVMAFDRDGEKALDISVNMVYEDININGALKLVF 60

PCT-US93-03076-10

PCT-US93-03076-2

Query Match 6.5%; Score 210; DB 5; Length 1513;
Best Local Similarity 19.1%; Pred. No. 4.5e-10;
Matches 125; Conservative 99; Mismatches 224; Indels 208; Gaps 27;

SEQ ID NO 15
LENGTH: 547
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: OTHER INFORMATION: 2471716CD1
US-09-855-323-15

Query Match 6.6%; Score 214.5; DB 4; Length 547;
Best Local Similarity 29.2%; Pred. No. 3e-11; Matches 57; Conservative 34; Mismatches 75; Indels 29; Gaps 3;

QY 349 GMLADPV-----SQTSPMPSIVHCMNEIEQRLGTLTGLYRISGCPRTYKELKEK 399
Db 330 GLIRDOVFGCQLESLCOREGDPVPSFLRLCIAVDKRGKLDYDGIYRVSGNLAQVQKRLF 389

QY 400 FLRKVQVPL-----LSKUDIHAICSLKJFLKJENLJKEPLTFLRNR 440
Db 390 VDRERAVTSRDRYVFPEQPGQGRGLDSTENDIHWGALKFLRELPQPLVPLLP 449

QY 441 AFMEAAABITDEDSNIAAMQAVGELPOANRDTLAFMLHQLY-AOSPHTKDQVANLAKV 499
Db 450 HPRALALISESSEQCLSQIQLIGMSMPKENDHDTYLUHLRVIANSKDNRTPHNGIV 509

QY 500 FGPTIVAHAVNPDD 514
Db 510 FGPTLFRPQEQTSDP 524

RESULT 7

PCT-US93-03076-2

Sequence 2, Application PC/TUS9303076

GENERAL INFORMATION:

APPLICANT: Whitehead Institute for Biomedical Research

TITLE OF INVENTION: GAP Associated Protein p190 and

TITLE OF SEQUENCES: 20

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: 2 Militia Drive

CITY: Lexington

STATE: MA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIA TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/03076

FILE REFERENCE: 19930331

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Retricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: WHI92-03A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1513 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

ORGANISM: Homo sapiens

FEATURE: OTHER INFORMATION: 2471716CD1

RESULT 8

US-09-538-092-1230

Sequence 1230, Application US/09538092

PATENT NO. 6753314

GENERAL INFORMATION:

APPLICANT: Gloc, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR FILING DATE: 1999-04-01

PRIOR APPLICATION NUMBER: 60/178,965

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9

SEQ ID NO 1230

LENGTH: 946

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: OTHER INFORMATION: 2471716CD1

; NAME/KEY: misc_feature
 ; LOCATION: (0)..(0)
 ; OTHER INFORMATION: Polypeptide Accession Number P98171
 ; US-09-538-092-1230

Query Match Best Local Similarity 21.4%; Score 202.5; DB 4; Length 946; Matches 143; Conservative 99; Mismatches 256; Indels 170; Gaps 27;

Qy 45 QRTDH--BLG---KYKDLMAKERTSALDVKLKHARNQVQEIKRQRAEADCEKLE 97
 Db 130 RQSHSHTAEDVGRVKSISDLEQDLEEVNSBLQATKTYQAHMSEVNAZKLRKAE 189

Qy 98 RQDQ-LAREMLMDTGSIQLSBEQKSAL-----AFLNRGQPSSSNAGNKRST 145
 Db 190 RQEKRAGRSVRSPPTAGATEAGLURKSSLKKGRLVERKQAKMENHUKCTKARNEVLS 249

Qy 146 IDDEGTSILSDISFDKTDSELDWMDSSLVLKTFKLKKEKREKRSTSRQFVDPGPPGVKTSIG 205
 Db 250 L---ASVNAVANVSYLHDVLDLMDCCDTGFHLALGQVRSYTAESRTQASQVQGLGSLE 306

Qy 206 SAVD---QGENESIVAKTTV-----INDGGIEAV----- 233
 Db 307 EATVADLDPGDKAKVLETHATVCPPLADYHHDGEVAEICVEMELDELUPRAONIQ 366

Qy 234 -----STIBTPVPTRSRRTKGTLQPM-----NSDSTLNSRQLPRTETDSVGTPOSNG 282
 Db 367 SRUDRQTTETEEV---NKTAKLQALLEVAVASDDGVDLSFGTSPSTE--SUKSTSDDP 421

Qy 283 GMR-----LHDVFVSKTIVKRESCVPGKRIKFGKLSK----- 315
 Db 422 GSRQAGRRQQOBETEFLKUQBYLS-----GRSI-LAKLQAKHEKHLQBAL 468

Qy 316 --CRDCRVSHREC-----RURCPCLI--PTLIGTPVKIGEGMFLADFVQSOTSPMP 363
 Db 469 QRDKEEBSVMSVTOYTORKEKQEROPRISQYMQRLFG-----GDEKEFTQSSGPVP 521

Qy 364 SIVVHCVNIEQGLITEROLYRISGCDRTVKELKEFLRKVTKVPLS--KVDIHAICSL 421
 Db 522 LUVESCTRPININGLQHSGIFRVSQAGQIVRSERDAFERGED-PLVSGCTAHLDSVAGV 580

Qy 422 LKQFLRNKLEPLTFRNRAFMEAETTBDNSIAAMYQAVGELQUPQANRDTAFLMTHLQ 481
 Db 581 LKLYFRSLEPPLFPFDLFGELLASELDTAERVEHVSRLWLPAPVILVRLYLFPLN 640

Qy 482 RYQO-SPPTKMDYANLAKVFGPTIVAHAVPNPPVPTMSQDIKQPKVUERLUSPLEWNS 540
 Db 641 HLUQYSDENMDPYNLAVCFGPML-----PVAGQDPVQALQGRINQLOV----- 684

Qy 541 QFMVNEQENIDPLHVIENSNAFSTPQTPDIKVSLGLGPVTPHEQHLLKTPSSSSLSQ-RVR 599
 Db 685 QTLIVOPDRVFP-----PLT-----SLPGPV--YEKCMAPPSCIGDAGLE 724

Qy 600 STLTKNTP 607
 Db 725 SLGADNDP 732

RESULT 9
 US-10-164-595-40
 ; Sequence 40, Application US/10164595
 ; Patent No. 6657054
 ; GENERAL INFORMATION:
 ; APPLICANT: Origene Technologies, Inc
 ; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
 ; FILE REFERENCE: IU 103 R1
 ; CURRENT APPLICATION NUMBER: US/10/164 595
 ; CURRENT FILING DATE: 2002-06-10
 ; NUMBER OF SEQ ID NOS: 80
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 40
 ; LENGTH: 645
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-164-595-40

Query Match Best Local Similarity 20.2%; Score 198.5; DB 4; Length 645; Matches 96; Conservative 77; Mismatches 14; Indels 129; Gaps 18;

Qy 166 DWDSLVLVTKFLKKEKREKRSTSRQFVDPGPPGVKTKTSIGSAVDQGNSIVAKTTVVPN 225
 Db 8 NWBD-----FNLYKEAAKARSRSWMT-----EOMAFAHPSSTPN 42

Qy 226 DGGPIEVAVSTIETVPTWRSRRTKGTLQPNWNSDSTLNSRQLPRTETDSVGPQNSGMR 285
 Db 43 --PLERIKMG--WIKKQR--SIVKQW-----QORYFVRAQ-----Q 74

Qy 286 LHDVFVSKTIVKRESCVPGKRIKFGKLSKGRDCRVSHPBCDRDPLPCPT----- 338
 Db 75 LYKVKBEDTKPGCMMWPGCTIK-----EATNPBAGKVFELIPASWMDQNR 123

Qy 339 -----LIGTPVKIGEGMFLADFVQSOTSP---MIPSIVHIC 369
 Db 124 MGDSYVLMASSQAEEMBWEWVKLRLRVAGTPCCVPGFQGDLDETVAEYQFGPHLVLVEK 183

; CURRENT APPLICATION NUMBER: US/09/854,133
 ; CURRENT FILING DATE: 2001-05-11

RESULT 11
 US-10-164-595-73
 ; Sequence 73, Application US/10164595
 ; Patent No. 6657054
 ; GENERAL INFORMATION:
 ; APPLICANT: Origene Technologies, Inc
 ; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
 ; FILE REFERENCE: IJU 103 R1
 ; CURRENT APPLICATION NUMBER: US/10/164,595
 ; CURRENT FILING DATE: 2002-06-10
 ; NUMBER OF SEQ ID NOS: 80
 ; SEQ ID NO 73
 ; LENGTH: 638
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-164-595-73

Query Match 6.1%; Score 197.5; DB 4; Length 638;
 Best Local Similarity 24.5%; Pred. No. 1.6e-09;
 Matches 66; Conservative 53; Mismatches 117; Indels 33; Gaps 8;

QY 341 GTPVKRIGKGMGLAPFVPSQFSP---MIPSIVVHCVNENETQRGILTGLYRISGCDTVEL 396
 Db 144 GTPCGVGFGORLDETFVAYEOKRGPHLIVPLIVEKCAFILEHGRNEEGFRIPQGDNLVQQL 203

QY 397 KERFLRUKVWPLSKVVDIHAATCSLLKPLKPLRNKEPLTFLRUMRAFMEAETIDEDNSIA 456
 Db 204 RDAF-DAGERPSFDRTDVTWASLKLQYLRDLPFEPVWPSQYEGFLLGQLINADEAKA 262

QY 457 -AMYQANGELPQANDTFLAFLMLHORY-AOSPHTRKDVANLAKVFGPTIVAHAVNPD 513
 Db 263 QSEIMKQLSILPDRDYNLSIYICRFELHQLNCAWKNSVNDLATVIGNLRSKVEP- 321

QY 514 PVTMSQDTRKQPKVVERLISLPLEYWSQPMVWQBTI-----DPLAVIENSNAFSTPQ 566
 Db 322 -----AVIMRGTPOIQRWT-----MMIRDHEVLPKSKDIPISPPAQKN--DPK 364

QY 567 TPDIKVSLQGPPVTPPEHQQLKTSSSL 595
 Db 365 KAPVARSSVGDATEDLRLISRTSDSSMT 393

RESULT 12
 US-09-270-767-32573
 ; Sequence 32573, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 4790
 ; LENGTH: 537
 ; TYPE: PRT
 ; ORGANISM: *Drosophila melanogaster*
 ; US-09-270-767-47790

Query Match 6.0%; Score 195.5; DB 4; Length 537;
 Best Local Similarity 22.5%; Pred. No. 1.9e-09;
 Matches 92; Conservative 66; Mismatches 172; Indels 79; Gaps 17;

QY 258 DSTLNRSQLEPRTEDSVGPTQSGNGMLHDPVSKTVKPE-----CVPCCR- 306
 Db 128 DSTNTAVLVLNSNTSDVCCSSNSSSGG-----SPAVGRSKSGDRRNGLECCSSKRW 180

QY 307 -IKFGKUSLKRCDRCV-----HPECRDRCLPCLPCTPLGTPVKI-----GEGMLAD 353
 Db 181 HDLKLORMHTE-QDLYVQTTYSQEBQSKQP-TLAPEGGLDPEVQVQBOQBTORGNRGCGNS 238

QY 354 FVQSTP-----MIPSIVVHCVNENETQRGILTGLYRISGCDTVEL-----GLYRISGCDTVEL 393
 Db 239 ASSTTKPCFDTLEMLVHDKQRTVPIWDCDLPQKRYSTQPIEGIVHQCGDNKI 298

QY 394 KELKEKFLRUKVWPLSKVVDIHAATCSLLKPLKPLRNKEPLTFLRUMRAFMEAETIT 449
 Db 299 QTLRFS-IDANYYDSLRQPDVHDTLTCVGLKFLREIKSPVTRNNEAKTETGQPNQMLT 357

QY 450 DEPDNSTIAMYQVGLPQANRDTFLAFLMLHORY-AOSPHTRKDVANLAKVFGPTIVAHAV 509
 Db 358 DISAKLDSLKRLJRSLSPESNRDMDYFGHFRITKVPLOQSAETISISTPSIF-HIV 416

QY 510 PVPDPVMSQDTRKQPKVVERLISLPLEYWSQFM--MVEQENIDPLHVI--ENSAFST 564
 Db 417 PGCVHMDPQDQOLIREGEBTLDCCVQLKMLVEYQGRIFDRURPHRPNRSPTWAVANGSGNPLRN 476

QY 565 PVPDPDTRKQPKVVERLISLPLEYWSQFM-----PEHOLKTPSSSLSS 525
 Db 477 PEIPSTRKRPETQIVPLATTSVYPPNSPNRSPKSWFSKIPSSHTRYRI 525

RESULT 13
 US-09-270-767-47790
 ; Sequence 47790, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 4790
 ; LENGTH: 537
 ; TYPE: PRT
 ; ORGANISM: *Drosophila melanogaster*
 ; US-09-270-767-47790

Query Match 6.0%; Score 195.5; DB 4; Length 537;
 Best Local Similarity 22.5%; Pred. No. 1.9e-09;
 Matches 92; Conservative 66; Mismatches 172; Indels 79; Gaps 17;

QY 258 DSTLNRSQLEPRTEDSVGPTQSGNGMLHDPVSKTVKPE-----CVPCCR- 306
 Db 128 DSTNTAVLVLNSNTSDVCCSSNSSSGG-----SPAVGRSKSGDRRNGLECCSSKRW 180

QY 307 -IKFGKUSLKRCDRCV-----HPECRDRCLPCLPCTPLGTPVKI-----GEGMLAD 353
 Db 181 HDLKLORMHTE-QDLYVQTTYSQEBQSKQP-TLAPEGGLDPEVQVQBOQBTORGNRGCGNS 238

QY 354 FVQSTP-----MIPSIVVHCVNENETQRGILTGLYRISGCDTVEL-----GLYRISGCDTVEL 393
 Db 239 ASSTTKPCFDTLEMLVHDKQRTVPIWDCDLPQKRYSTQPIEGIVHQCGDNKI 298

QY 394 KELKEKFLRUKVWPLSKVVDIHAATCSLLKPLKPLRNKEPLTFLRUMRAFMEAETIT 449
 Db 299 QTLRFS-IDANYYDSLRQPDVHDTLTCVGLKFLREIKSPVTRNNEAKTETGQPNQMLT 357

QY 450 DEENSIAMYQAVGELPOANRDTAFLMHQLQRAQSPTKMDVANLAKVFGPTIVAHV 509 ; FILE REFERENCE: PC-0010 US
 ; Sequence 32, Application US/09507765 ; CURRENT APPLICATION NUMBER: US/09/507,765
 ; Patent No. 6509155 ; CURRENT FILING DATE: 2000-02-18
 ; GENERAL INFORMATION: ; NUMBER OF SEQ ID NOS: 33
 ; APPLICANT: Klinger, Tod M. ; SOFTWARE: PERL Program
 ; APPLICANT: Stewart, Elizabeth A. ; SEQ ID NO: 30
 ; APPLICANT: Yue, Henry ; LENGTH: 433
 ; APPLICANT: Baughn, Mariah R. ; TVBR: PRT
 ; TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS ; ORGANISM: Homo sapiens
 ; FILE REFERENCE: PC-0010 US ; FEATURE:
 ; CURRENT APPLICATION NUMBER: US/09/507,765 ; NAME/KEY: misc feature
 ; CURRENT FILING DATE: 2000-02-18 ; OTHER INFORMATION: Incyte ID No. 6509155 3068538CD1
 ; NUMBER OF SEQ ID NOS: 33 ; US-09-507-765-30
 ; SOFTWARE: ERL Program

Db 417 PQQVHMQDIQQLREGETIADCVKLMLEYQGRIFDRLRPHPRSPPTAWAVANGSGNPLRN 476

QY 565 PQPDIK---VSLIGPVTT-----BHQHLCPPSSSSLGSRV 598

Db 477 PELPSTRPTEPQLVPLATTSYPNSPNSRYPKSWSKIPGSHTRYR 525

RESULT 14 ; US-09-507-765-32

; Sequence 32, Application US/09507765

; Patent No. 6509155

; GENERAL INFORMATION:

; APPLICANT: Klinger, Tod M.

; APPLICANT: Stewart, Elizabeth A.

; APPLICANT: Yue, Henry

; APPLICANT: Baughn, Mariah R.

; TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS

QY 325 PCCRDRPRLCPT-LGTPVKIGEGMLADFVQSQTSPMPSIVHCVNEISQRGLTETGL 383 ; FILE REFERENCE: PC-0010 US
 ; Sequence 32, Application US/09507765 ; CURRENT APPLICATION NUMBER: US/09/507,765
 ; Patent No. 6509155 ; CURRENT FILING DATE: 2000-02-18
 ; NUMBER OF SEQ ID NOS: 33 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: ERL Program

Db 177 PPTKTPPRPPLPTQGTVSLQ---YIKD--KNQGBLIPPLRFTVYLREKGRLRTEGL 230

QY 384 YRISGCRTVKSLKEKLRVKVPLSKVVDIHAICSLKLDRNLKEPLUTPRLNRAFM 443

Db 231 FRRSASVQTVREIQLRNQGVN-FDQYGDHTIPAVILKTFRLPRLPQLTFF--QAYE 286

QY 444 EAABTBDNS--IAAMYQAVGELPOANRDTAFLMHQLQRA-QSPTKMDVANLAKV 500

Db 287 QIGITCVESLRVGGQILRSPLERNYVYVRLYMGFLHAVSRESIFNKKMISNLACVF 346

QY 501 GPTIVAHAVPNEDPVUTMSODIKRQPKVYERLISLPLEYWSQFMMVFGCENIDPLHVIENSN 560

Db 347 GLNL-----IWPSQVSSLSALV-----PLMFTELLIEYEKI----- 380

QY 561 ASSTPQTPDIKVSLLGIVTTPHEQLL-----KTPSSSSLQRVRSVLTKOT 606

Db 381 -FSTPEAPG-----BHLGLAPWEGSRAAPLQEAVPRTQATGLTKPT 420

RESULT 15 ; US-09-507-765-30

; Sequence 30, Application US/09507765

; Patent No. 6509155

; GENERAL INFORMATION:

; APPLICANT: Klinger, Tod M.

; APPLICANT: Stewart, Elizabeth A.

; APPLICANT: Yue, Henry

; APPLICANT: Baughn, Mariah R.

; TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS

QY 325 PCCRDRPRLCPT-LGTPVKIGEGMLADFVQSQTSPMPSIVHCVNEISQRGLTETGL 383 ; FILE REFERENCE: PC-0010 US
 ; Sequence 32, Application US/09507765 ; CURRENT APPLICATION NUMBER: US/09/507,765
 ; Patent No. 6509155 ; CURRENT FILING DATE: 2000-02-18
 ; NUMBER OF SEQ ID NOS: 33 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: ERL Program

Db 77 PPTKTPPRPPLPTQGTVSLQ---YIKD--KNQGBLIPPLRFTVYLREKGRLRTEGL 230

QY 384 YRISGCRTVKSLKEKLRVKVPLSKVVDIHAICSLKLDRNLKEPLUTPRLNRAFM 443

Db 131 FRRSASVQTVREIQLRNQGVN-FDQYGDHTIPAVILKTFRLPRLPQLTFF--QAYE 186

QY 444 EAABTBDNS--IAAMYQAVGELPOANRDTAFLMHQLQRA-QSPTKMDVANLAKV 500

Db 187 QIGITCVESLRVGGQILRSPLERNYVYVRLYMGFLHAVSRESIFNKKMISNLACVF 246

QY 501 GPTIVAHAVPNEDPVUTMSODIKRQPKVYERLISLPLEYWSQFMMVFGCENIDPLHVIENSN 560

Db 247 GLNL-----IWPSQVSSLSALV-----PLMFTELLIEYEKI----- 280

QY 561 ASSTPQTPDIKVSLLGIVTTPHEQLL-----KTPSSSSLQRVRSVLTKOT 606

Db 281 -FSTPEAPG-----BHLGLAPWEGSRAAPLQEAVPRTQATGLTKPT 320

RESULT 15 ; US-09-507-765-30

; Sequence 30, Application US/09507765

; Patent No. 6509155

; GENERAL INFORMATION:

; APPLICANT: Klinger, Tod M.

; APPLICANT: Stewart, Elizabeth A.

; APPLICANT: Yue, Henry

; APPLICANT: Baughn, Mariah R.

; TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS

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QY	121	OKSALAFLNRLNRGOPSSNAGNKLSTIDESGSLTSDISFDKIDESLDWSSLVTKLKKR	RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalius D.E., Schein J.B., Jones S.J., Marr A.M., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
Db	121	OKSALAFLNRLNRGOPSSNAGNKLSTIDESGSLTSDISFDKIDESLDWSSLVTKLKKR	RA	RA
QY	181	EKRSTSRQFVQPGPGVKTRSIGSAVDQGENESTVAKTTVTPNDGGPIEAUSTETVP	RA	RT
Db	181	EKRSTSRQFVQPGPGVKTRSIGSAVDQGENESTVAKTTVTPNDGGPIEAUSTETVP	RA	RT
QY	241	YWRSRKTRGTLQPNSDSTANSRQEPRTEIDSVGTPQSGMRLJDVFUSKVKEFESC	RA	RT
Db	241	YWRSRKTRGTLQPNSDSTANSRQEPRTEIDSVGTPQSGMRLJDVFUSKVKEFESC	RA	RT
QY	301	VPGKRRKFGKLSKCRDRVSHPECRDRCLPCIPFLGTPVKIGGMLADFSQTP	RA	RN
Db	301	VPGKRRKFGKLSKCRDRVSHPECRDRCLPCIPFLGTPVKIGGMLADFSQTP	RA	RN
QY	361	MPSIVHCVNIEORGTLTGYRISGCDRTYKEKEKLRVKTPLSKVDDHAIICS	RA	RC
Db	361	MPSIVHCVNIEORGTLTGYRISGCDRTYKEKEKLRVKTPLSKVDDHAIICS	RA	RC
QY	361	MPSIVHCVNIEORGTLTGYRISGCDRTYKEKEKLRVKTPLSKVDDHAIICS	RA	RC
Db	361	MPSIVHCVNIEORGTLTGYRISGCDRTYKEKEKLRVKTPLSKVDDHAIICS	RA	RC
QY	421	LKDFLNRLKEPLTFLNRAFMAETEDNSIAAMYQAVGELPQANRDLAFMHL	RA	RN
Db	421	LKDFLNRLKEPLTFLNRAFMAETEDNSIAAMYQAVGELPQANRDLAFMHL	RA	RN
QY	481	QVAQSPHTKMDVANLAKVFGPTIVAHAVNPDPVMSQDKRQPKVVERLISLPLBWS	RA	RN
Db	481	QVAQSPHTKMDVANLAKVFGPTIVAHAVNPDPVMSQDKRQPKVVERLISLPLBWS	RA	RN
QY	541	QPMVGEENIDPHYNSNASTPQDPKVLGTTPHOLIKTPSSSLSPQRS	RA	RN
Db	541	QPMVGEENIDPHYNSNASTPQDPKVLGTTPHOLIKTPSSSLSPQRS	RA	RN
QY	601	TLTKNTPRFGSKSATNLGRQNFASPMLK	RA	RN
Db	601	TLTKNTPRFGSKSATNLGRQNFASPMLK	RA	RN
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ID	O9H05	PRELIMINARY; PRT; 632 AA.		
AC	O9H05;			
DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS	Homo sapiens (Human);			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX				
NCBI_TAXID=9606;				
RN	[1]			
SEQUENCE FROM N.A.				
RC				
RA	TTTGT=Testis; Pousta A., Klein M., Mewes H.W., Gassenhuber J., Niemann S.; RRL submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.			
RN	[2]			
SEQUENCE FROM N.A.				
RC				
RX	MEDLINE=22388257; PubMed=1247932;			
RA	Strasser R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkin R.F., Jordan H., Moore T., Max S.I., Rubin W.J., Hsieh F., Diatchenko L., Marusina A.A., Farmer G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.E., Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C., Raha S.S., Loquai Lano N.A., Peters G.J., Abramson R.D., Mulahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon C.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.S.,			
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ID	Q9H05	PRELIMINARY; PRT; 632 AA.		
AC	O9H05;			
DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS				
OC				
OX				
NCBI_TAXID=9606;				
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RC				
RX	SEQUENCE FROM N.A.			
RA	TTTGT=Testis; MEDLINE=22388257; PubMed=1247932;			
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DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS				
OC				
OX				
NCBI_TAXID=9606;				
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SEQUENCE FROM N.A.				
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RX	SEQUENCE FROM N.A.			
RA	TTTGT=Testis; MEDLINE=22388257; PubMed=1247932;			
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AC	Q9H05;			
DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS				
OC				
OX				
NCBI_TAXID=9606;				
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RX	SEQUENCE FROM N.A.			
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ID	Q9H05	PRELIMINARY; PRT; 632 AA.		
AC	Q9H05;			
DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS				
OC				
OX				
NCBI_TAXID=9606;				
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RX	SEQUENCE FROM N.A.			
RA	TTTGT=Testis; MEDLINE=22388257; PubMed=1247932;			
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ID	Q9H05	PRELIMINARY; PRT; 632 AA.		
AC	Q9H05;			
DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS				
OC				
OX				
NCBI_TAXID=9606;				
RN	[1]			
SEQUENCE FROM N.A.				
RC				
RX	SEQUENCE FROM N.A.			
RA	TTTGT=Testis; MEDLINE=22388257; PubMed=1247932;			
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ID	Q9H05	PRELIMINARY; PRT; 632 AA.		
AC	Q9H05;			
DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS				
OC				
OX				
NCBI_TAXID=9606;				
RN	[1]			
SEQUENCE FROM N.A.				
RC				
RX	SEQUENCE FROM N.A.			
RA	TTTGT=Testis; MEDLINE=22388257; PubMed=1247932;			
Q9H05				
ID	Q9H05	PRELIMINARY; PRT; 632 AA.		
AC	Q9H05;			
DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS				
OC				
OX				
NCBI_TAXID=9606;				
RN	[1]			
SEQUENCE FROM N.A.				
RC				
RX	SEQUENCE FROM N.A.			
RA	TTTGT=Testis; MEDLINE=22388257; PubMed=1247932;			
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ID	Q9H05	PRELIMINARY; PRT; 632 AA.		
AC	Q9H05;			
DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS				
OC				
OX				
NCBI_TAXID=9606;				
RN	[1]			
SEQUENCE FROM N.A.				
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RX	SEQUENCE FROM N.A.			
RA	TTTGT=Testis; MEDLINE=22388257; PubMed=1247932;			
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ID	Q9H05	PRELIMINARY; PRT; 632 AA.		
AC	Q9H05;			
DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS				
OC				
OX				
NCBI_TAXID=9606;				
RN	[1]			
SEQUENCE FROM N.A.				
RC				
RX	SEQUENCE FROM N.A.			
RA	TTTGT=Testis; MEDLINE=22388257; PubMed=1247932;			
Q9H05				
ID	Q9H05	PRELIMINARY; PRT; 632 AA.		
AC	Q9H05;			
DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS				
OC				
OX				
NCBI_TAXID=9606;				
RN	[1]			
SEQUENCE FROM N.A.				
RC				
RX	SEQUENCE FROM N.A.			
RA	TTTGT=Testis; MEDLINE=22388257; PubMed=1247932;			
Q9H05				
ID	Q9H05	PRELIMINARY; PRT; 632 AA.		
AC	Q9H05;			
DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS				
OC				
OX				
NCBI_TAXID=9606;				
RN	[1]			
SEQUENCE FROM N.A.				
RC				
RX	SEQUENCE FROM N.A.			
RA	TTTGT=Testis; MEDLINE=22388257; PubMed=1247932;			
Q9H05				
ID	Q9H05	PRELIMINARY; PRT; 632 AA.		
AC	Q9H05;			
DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS				
OC				
OX				
NCBI_TAXID=9606;				
RN	[1]			
SEQUENCE FROM N.A.				
RC				
RX	SEQUENCE FROM N.A.			
RA	TTTGT=Testis; MEDLINE=22388257; PubMed=1247932;			
Q9H05				
ID	Q9H05	PRELIMINARY; PRT; 632 AA.		
AC	Q9H05;			
DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS				
OC				
OX				
NCBI_TAXID=9606;				
RN	[1]			
SEQUENCE FROM N.A.				
RC				
RX	SEQUENCE FROM N.A.			
RA	TTTGT=Testis; MEDLINE=22388257; PubMed=1247932;			
Q9H05				
ID	Q9H05	PRELIMINARY; PRT; 632 AA.		
AC	Q9H05;			
DT	01-MAR-2001 (TREMBL; 16, Last sequence update)			
DT	01-OCT-2004 (T-EMBL; 28, Last annotation update)			
DE	Hypothetical protein DKF26434C011 (RACGAP1 protein).			
GN	Name-DKF26434C011; Synonyms=RACGAP1;			
OS				

Db	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480	Qy	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
Qy	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540	Db	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
Db	481	ORVAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540	Qy	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
Qy	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600	Db	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
Db	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600	Qy	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
Qy	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632	Db	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
Db	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632	Qy	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
Qy	[1]	SEQUENCE FROM N.A.		Db	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
AC	Q9NNW2	PRELIMINARY;	PRT;	Qy	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DT	01-OCT-2000	(TREMBLrel. 15, Created)		Db	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)		Qy	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DE	01-MAR-2004	(TREMBLrel. 25, Last annotation update)		Db	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DE	Hypothetical protein	FLJ20726;		Qy	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632
OS	Homo sapiens (Human)			Db	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632
OC	Bukarvota; Metacoda; Chordata; Craniata; Vertebrata; Euteleostomi;			Qy	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			Db	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
OX	NCBI_TaxID=9606;			Qy	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
RN	[1]	SEQUENCE FROM N.A.		Db	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
RP	RA	Kawakami T., Noguchi S., Itoh T., Shigeita K., Senba T., Matsumura K.,		Qy	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
RA	RA	Nakajima Y., Mizuno T., Moriga M., Ota T., Suzuki Y., Obayashi M.,		Db	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
RA	RA	Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.,		Qy	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
RL	RL	Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.		Db	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
DR	DR	EMBL; AB00733; BAA91347.1;		Qy	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
DR	DR	HSSP; Q98935; 1P7C.		Db	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
DR	DR	GO; GO:0005489; F:electron transporter activity; IEA.		Qy	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	GO; GO:005506; F:iron ion binding; IEA.		Db	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	GO; GO:005618; P:electron transport; IEA.		Qy	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	GO; GO:007242; P:intracellular signaling cascade; IEA.		Db	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	InterPro; IPR001450; 4Fe4S ferredoxin.		Qy	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DR	DR	InterPro; IPR00219; DAG PE-Bind.		Db	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DR	DR	InterPro; IPR00198; Rho_GAP.		Qy	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632
DR	DR	InterPro; IPR008936; Rho_GAP.		Db	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632
DR	DR	Pfam; PF00130; Cl_1; 1.		Qy	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	PRINTS; PR00353; 4Fe4S-ferredoxin.		Db	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	SMART; SM00109; Cl_1; 1.		Qy	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	SMART; SM00324; RhogAP; 1.		Db	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	SMART; SM00324; RhogAP; 1.		Qy	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
DR	DR	SMART; SM00324; RhogAP; 1.		Db	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
DR	DR	PROSITE; PS50238; Rho_GAP.		Qy	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
DR	DR	SEQUENCE FROM N.A.		Db	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
DR	DR	SEQUENCE FROM N.A.		Qy	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
DR	DR	SEQUENCE FROM N.A.		Db	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
DR	DR	SEQUENCE FROM N.A.		Qy	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	SEQUENCE FROM N.A.		Db	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	SEQUENCE FROM N.A.		Qy	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	SEQUENCE FROM N.A.		Db	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	SEQUENCE FROM N.A.		Qy	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DR	DR	SEQUENCE FROM N.A.		Db	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DR	DR	SEQUENCE FROM N.A.		Qy	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632
DR	DR	SEQUENCE FROM N.A.		Db	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632
DR	DR	SEQUENCE FROM N.A.		Qy	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
DR	DR	SEQUENCE FROM N.A.		Db	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
DR	DR	SEQUENCE FROM N.A.		Qy	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
DR	DR	SEQUENCE FROM N.A.		Db	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
DR	DR	SEQUENCE FROM N.A.		Qy	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
DR	DR	SEQUENCE FROM N.A.		Db	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
DR	DR	SEQUENCE FROM N.A.		Qy	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	SEQUENCE FROM N.A.		Db	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	SEQUENCE FROM N.A.		Qy	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	SEQUENCE FROM N.A.		Db	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	SEQUENCE FROM N.A.		Qy	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DR	DR	SEQUENCE FROM N.A.		Db	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DR	DR	SEQUENCE FROM N.A.		Qy	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632
DR	DR	SEQUENCE FROM N.A.		Db	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632
DR	DR	SEQUENCE FROM N.A.		Qy	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
DR	DR	SEQUENCE FROM N.A.		Db	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
DR	DR	SEQUENCE FROM N.A.		Qy	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
DR	DR	SEQUENCE FROM N.A.		Db	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
DR	DR	SEQUENCE FROM N.A.		Qy	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
DR	DR	SEQUENCE FROM N.A.		Db	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
DR	DR	SEQUENCE FROM N.A.		Qy	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	SEQUENCE FROM N.A.		Db	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	SEQUENCE FROM N.A.		Qy	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	SEQUENCE FROM N.A.		Db	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	SEQUENCE FROM N.A.		Qy	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DR	DR	SEQUENCE FROM N.A.		Db	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DR	DR	SEQUENCE FROM N.A.		Qy	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632
DR	DR	SEQUENCE FROM N.A.		Db	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632
DR	DR	SEQUENCE FROM N.A.		Qy	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
DR	DR	SEQUENCE FROM N.A.		Db	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
DR	DR	SEQUENCE FROM N.A.		Qy	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
DR	DR	SEQUENCE FROM N.A.		Db	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
DR	DR	SEQUENCE FROM N.A.		Qy	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
DR	DR	SEQUENCE FROM N.A.		Db	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
DR	DR	SEQUENCE FROM N.A.		Qy	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	SEQUENCE FROM N.A.		Db	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	SEQUENCE FROM N.A.		Qy	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	SEQUENCE FROM N.A.		Db	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	SEQUENCE FROM N.A.		Qy	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DR	DR	SEQUENCE FROM N.A.		Db	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DR	DR	SEQUENCE FROM N.A.		Qy	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632
DR	DR	SEQUENCE FROM N.A.		Db	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632
DR	DR	SEQUENCE FROM N.A.		Qy	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
DR	DR	SEQUENCE FROM N.A.		Db	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
DR	DR	SEQUENCE FROM N.A.		Qy	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
DR	DR	SEQUENCE FROM N.A.		Db	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
DR	DR	SEQUENCE FROM N.A.		Qy	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
DR	DR	SEQUENCE FROM N.A.		Db	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
DR	DR	SEQUENCE FROM N.A.		Qy	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	SEQUENCE FROM N.A.		Db	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	SEQUENCE FROM N.A.		Qy	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	SEQUENCE FROM N.A.		Db	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	SEQUENCE FROM N.A.		Qy	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DR	DR	SEQUENCE FROM N.A.		Db	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DR	DR	SEQUENCE FROM N.A.		Qy	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632
DR	DR	SEQUENCE FROM N.A.		Db	601	TLTKNTRPGSKSKSATNLGRQGNFFASPMLK	632
DR	DR	SEQUENCE FROM N.A.		Qy	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
DR	DR	SEQUENCE FROM N.A.		Db	241	YWRTRSRKRKTQIOPWNDSITNSRQLPRTEDTSVGTPOSNGMRLIDFVSKTVIKPESC	300
DR	DR	SEQUENCE FROM N.A.		Qy	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
DR	DR	SEQUENCE FROM N.A.		Db	301	VPGKRKIKFGKSLKCDCRVSHPGCRDRCLPCPCTLIGPVKQGEGMLADFVSTSP	360
DR	DR	SEQUENCE FROM N.A.		Qy	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
DR	DR	SEQUENCE FROM N.A.		Db	361	MPSIVVHCVNIEQRGTEGTYSGCDRTVKELEKFLRKVTVLISKVDDHACIS	420
DR	DR	SEQUENCE FROM N.A.		Qy	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	SEQUENCE FROM N.A.		Db	421	LLKDFLRLKEPLTFRINRRAFMEAETDEDSIAMIYQAVGELPQANRDTLAFMTHL	480
DR	DR	SEQUENCE FROM N.A.		Qy	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	SEQUENCE FROM N.A.		Db	481	QRAQASPTIKMDVANLAKVFGPTIVAHAVNPDPVTWSQDIKRQPKVVERLLSPLPEWS	540
DR	DR	SEQUENCE FROM N.A.		Qy	541	QFMVVEGENDIDPLHVINNSNASTPQDPDIKVLGPTPEHOLKTPSSSLQRVRS	600
DR	DR	SEQUENCE FROM N.A.		Db	541	QFM	

Matches	569;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	63	TERSAJDVKLKHARNQDVVEKRRORAEADECEKLEROIOLTEMLMCDTSSQIOLSEEQK	122						
Db	1	TERSAJDVKLKHARNQDVVEKRRORAEADECEKLEROIOLREMLMCDTSSQIOLSEEQK	60						
QY	123	SALAFLNQGQSSSNAGNKRSTIDESGSISLSDISFDKTDSDLWDSLLVTPKLUKREK	182						
Db	61	SALAFLNQGQSSSNAGNKRSTIDESGSISLSDISFDKTDSDLWDSLLVTPKLUKREK	120						
QY	183	RRSTSQFDPGPGPKTRSGSAQDGNSIVAKTIVTPNDGPEIAVSTIERTPYW	242						
Db	121	RKSTSQFVDGPGPKTRSGSAQDGNSIVAKTIVTPNDGPEIAVSTIERTPYW	180						
QY	243	TRSRRKIGTQDWNSTNSRQLEPRTETSVGTQSGNGMRLHDFVSKVVKPSCVP	302						
Db	181	TRSRRKIGTQDWNSTNSRQLEPRTETSVGTQSGNGMRLHDFVSKVVKPSCVP	240						
QY	363	PSIWHCVNEBORGUTETGYLRISSGDRTKELEKEFLRKRTVPLISKUDIATCSL	422						
Db	301	PSIWHCVNEBORGUTETGYLRISSGDRTKELEKEFLRKRTVPLISKUDIATCSL	360						
QY	423	KDFLRLNKEPLTFLRNLAFMEAETTBDNSIAAMQAVGELPQANRDTAFLMLHLQR	482						
Db	361	KDFLRLNKEPLTFLRNLAFMEAETTBDNSIAAMQAVGELPQANRDTAFLMLHLQR	420						
QY	483	WQSPHTRMDVANLAKVFGPTVVAHAVNPDPVTMLQDIKRQPKVVERLILSPLEYWSQF	542						
Db	421	WQSPHTRMDVANLAKVFGPTVVAHAVNPDPVTMLQDIKRQPKVVERLILSPLEYWSQF	480						
QY	543	MVEQEENIDPLHVIENSAFSPQTPKVLSSLGIVPVTPEHOLKLPKSSSLSQRTSL	602						
Db	481	MVEQEENIDPLHVIENSAFSPQTPKVLSSLGIVPVTPEHOLKLPKSSSLSQRTSL	540						
QY	603	TKNTPRFGSKKSATNLGRQGNFFASMLK	632						
Db	541	TKNTPRFGSKKSATNLGRQGNFFASMLK	570						

RESULT 5

Q9BZ74 PRELIMINARY; PRT; 628 AA.

ID Q9BZ74; AC 09BZ74; DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 25, Last annotation update)

DE PFKSG42; GN Name=PFKSG42;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606; OX [1] Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

RN SEQUENCE FROM N.A.

RA Wang, Y.-G.; Gong, L.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

RN EMBL; AF34184; AAC50293.1; -.

DR HSSP; Q9835; 1PFC.

DR InterPro; IPR00198; RhogAP.

DR InterPro; IPR00936; Rho_GAP.

DR Pfam; PF06520; RhogAP; 1.

DR SMART; SM00324; RhogAP; 1.

DR PROSITE; PS50238; RhogAP; 1.

SQ SEQUENCE; 628 AA; 70013 MW; A142955A613154CC CRC64;

RESULT 6

Q9WVML PRELIMINARY; PRT; 628 AA.

ID Q9WVML; AC 09WVML; DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)

DE Rac Gpase-activating protein (MgcRacGAP variant alpha) (MgcRacGAP variant beta) (Racgapt protein)

GN Name=Racgapt; Synonyms=MgcRacGAP;

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090; RN [1] SEQUENCE FROM N.A.

RN HSSP; Q9835; 1PFC.

RN Woolerton, E.J.; Hailotis, T.; Mueller, C.R.; "Identification and characterization of a transcript for a novel Rac Gpase-activating protein in terminally differentiating 3T3-L1 adipocytes";

RN DNA Cell Biol. 18:265-273 (1999).

RN [2] SEQUENCE FROM N.A.

RN MEDLINE=99249198; PubMed=10235109;

RA Kawashima, T.; Hirose, K.; Satoh, T.; Kaneko, A.; Ikeda, Y.; Kaziro, Y.; Nobasa, T.; Kitamura, T.; "MgcRacGAP is involved in the control of growth and differentiation of

Query Match 85.8%; Score 2781; DB 2; Length 628; Best Local Similarity 87.0%; Pred. No. 4; 6e-144; Matches 550; Conservative 31; Mismatches 47; Indels 4; Gaps 2;

Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	Db	479 LQRVAGSPDCKMDVSMILAKVFGPTLVGHAVIDPDPMTILQDTRPQMVNLRLSPALEW 538
RP	"Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative"; Dev. Dyn. 225:384-391(2002).	Db	539 NOQMMV-ENIDPNHIEINSVVFSTQTPDARVSMIGPLTPEQQMKTSSSSVQRMK 596
RC	TISSUE=Oocytes; MEDLINE=22341132; PubMed=12454917; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative"; Dev. Dyn. 225:384-391(2002).	Qy	540 SQMMVYEQENIDPLHVTEVNSAFASTQTQTPDITKVLISLGGVPTPEHQIKTSSSSVQVR 599
RL	RT	Db	539 NOQMMV-ENIDPNHIEINSVVFSTQTPDARVSMIGPLTPEQQMKTSSSSVQRMK 596
RN	[2]	RT	RT
RC	SEQUENCE FROM N.A.	RT	RT
RX	SEQUENCE FROM N.A.	RT	RT
RA	TISSUE=Oocytes; Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.	RT	RT
RL	EMBL; BC070771; AAH0771_1; -.	RT	RT
DR	InterPro; IPR01450; 4Fe4S ferredoxin.	RT	RT
DR	InterPro; IPR00219; DAG PE-bind.	RT	RT
DR	InterPro; IPR00198; RhoGAP.	RT	RT
DR	InterPro; IPR008936; Rho_GAP.	RT	RT
DR	PFam; PF0130; C1_1; 1.	RT	RT
DR	PFam; PF0620; RhoGAP; 1.	RT	RT
DR	PRINTS; PR00353; 4Fe4SFRDOXIN.	RT	RT
DR	SMART; SM00109; C1; 1.	RT	RT
DR	PROSITE; PS00479; DAG PE BIND_DOM; 1; 1.	RT	RT
DR	PROSITE; PS50081; DAG PE_BIND_DOM; 2; 1.	RT	RT
DR	PROSITE; PS50238; RhoGAP; 1; 1.	RT	RT
SO	SEQUENCE 629 AA; 70781 MW; 40BB97C1CHEADFC2 CRC64;	RT	RT
Query	Match	RESULT 8	RESULT 8
Best Local Similarity	76.1%; Pred. 1.8e-146;	AAH70771	AAH70771
Matches	482; Conservative 78; Mismatches 68; Indels 5; Gaps 4;	PRELIMINARY	PRELIMINARY
Qy	1 MDTMMILVNRNFIEQVRLVERVTESEGNEVQFOQLAKOFEDEFRKWORDHHEGKQKDLMK 60	RT	RT
Db	1 MATNLMLMLRNLFQQLMRQVQDGLNQEGIPQFQLAKOAKFEDFRRKWORSEHELMNKEMLMK 60	RT	RT
Qy	61 ABTERASALDVKLUKHARNQYDVEKRRRAEADCEKLERQIOLIREMLMD 60	RT	RT
Db	61 TETERSALLEVKLKHARNQYDVEKRRRAEADCEKLERQIOLIREMLMDPSGSEQ 120	RT	RT
Qy	121 QKSALATL-NRGCPSSNAGNKLSTIDESSESSILSDISFDKIDESLDWDSSILVKTFKLK 179	RT	RT
Db	121 QRSALANFLNTRQMSAQNGLGTRRLSTIDESASILSDISFDKIDESLDWDSSILVKTFKLK 180	RT	RT
Qy	180 REKRRSRQFVQDGGPPGVKURSISAVDODNESTVAKTTVTPNDGGPTEAVSTIETV 239	RT	RT
Db	181 REKRSRQFVQDGGPPGVKURSISAVDODNESTVAKTTVTPNDGGPTEAVSTIETV 239	RT	RT
Qy	240 PYWTRSRKRTGTLQPMNSDSTNSRQLEPRTRDSDVGTQPGNGMRLHDFFSKTVKPE 299	RT	RT
Db	240 PYNTRGRGRTGTLQPMNSDSSLASLRHLDKGEDTSQPO_NGGMRLHEFVSKTVKPE 298	RT	RT
Qy	300 CPGCKRIKFGKLSKLDRCRIVSHPCDRDQLPCLPCTLGPVKGEGMLADFSQTS 359	RT	RT
Db	299 CPGCKRIKFGKLSKLDRCRIVSHPCDRDQLPCLPCTLGPVKGEGMLADFSQTS 358	RT	RT
Qy	360 PMPIPSTIVVHCNIEQRLGTLGGLYRISGCDRIVKELKEKFLRKVTKVPLLSKVDTHAIC 419	RT	RT
Db	359 PMPIPIVVHCNIEQRLGGLYRISGCDRIVKELKEKFLRKVTKVPLLSKVDTHAIC 418	RT	RT
Qy	420 SLLKDFLRLNKEPLTFLRNFRAPEMEAETIDNSTMAMYVGLPQANRFLAFLMH 479	RT	RT
Db	419 GFLKDFLRLNKEPLTFLRNFRAPEMEAETIDNSTMAMYVGLPQANRFLAFLMH 478	RT	RT
Qy	480 LQVAGSPDCKMDVSMILAKVFGPTLVGHAVIDPDPMTILQDTRPQMVNLRLSPALEW 539	RT	RT
RC	SEQUENCE FROM N.A.	RT	RT
RA	Klein S., Strausberg R.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative"; Dev. Dyn. 225:384-391(2002).	RT	RT
RL	RT	RT	RT
RN	[3]	RT	RT
RC	SEQUENCE FROM N.A.	RT	RT
RX	SEQUENCE FROM N.A.	RT	RT
RA	TISSUE=Oocytes; Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.	RT	RT
RL	EMBL; BC070771; AAH0771_1; -.	RT	RT
DR	Hypothetical protein.	RT	RT
RW	SEQUENCE 629 AA; 70781 MW; 40BB97C1CHEADFC2 CRC64;	RT	RT
Query	Match	RESULT 8	RESULT 8
Best Local Similarity	76.1%; Pred. 1.8e-146;	AAH70771	AAH70771
Matches	482; Conservative 78; Mismatches 68; Indels 5; Gaps 4;	PRELIMINARY	PRELIMINARY
Qy	1 MDTMMILVNRNFIEQVRLVERVTESEGNEVQFOQLAKOFEDEFRKWORDHHEGKQKDLMK 60	RT	RT
Db	1 MATNLMLMLRNLFQQLMRQVQDGLNQEGIPQFQLAKOAKFEDFRRKWORSEHELMNKEMLMK 60	RT	RT

QY	61	AFTERSALDVULKHARNQDVDEIKRORAAECEKUERQIOLIREMLMDTSQIOLSEE	RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,' Butterfield Y.S.,
Db	61	TETERSLEVULKHARNQDVDEIKRORAAECEKUERQIOLIREMLMDTSQIOLSEQ	RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Krzywinski M.I., Skalska U., Jones S.J., Smailus D.E., Schnecko A., Schein J.E.,
QY	121	QKSALALI-NRGOPSSNAGNKLSTIDESGSTLSDISFDKIDESLDWSSILVKFLKK	RT	"Generation and initial analysis of more than 15,000 full-length human
Db	121	QKSALALI-NRGOPSSNAGNKLSTIDESGSTLSDISFDKIDESLDWSSILVKFLKK	RT	and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
QY	180	REKRSRSRQFVDPGPVKRSIGAVDQNEVAKTIVPVDGPGPTEAVSTIETV	RL	[2]
Db	180	REKRSRSRQFVDPGPVKRSIGAVDQNEVAKTIVPVDGPGPTEAVSTIETV	RL	SEQUENCE FROM N.A.
QY	181	REKRS-SRQHTEGPVPSKRNSIGAVDQNEVAKTIVPVDGPGPTEAVSTIETV	RA	TISSUE-Embryo; Klein S., Strauberg R.,
Db	181	REKRS-SRQHTEGPVPSKRNSIGAVDQNEVAKTIVPVDGPGPTEAVSTIETV	RA	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
QY	240	PWTRSRKRTGTLQPMNSDSTNSRQLEPRTRDSDVGTPOSQGMRLHDPSVTKPES	DR	EMBL: BC067994; AAH67994.1; -
Db	240	PWTRSRKRTGTLQPMNSDSTNSRQLEPRTRDSDVGTPOSQGMRLHDPSVTKPES	DR	InterPro: IPR01450; 4Fe4S ferredoxin.
QY	300	CYPCGKRITKFGKLSLKRDCRVSHPCCRDPCLPCLPTLIGTPVKIGEGLMADFQS	DR	InterPro: IPR00219; DAG PE-bind.
Db	300	CYPCGKRITKFGKLSLKRDCRVSHPCCRDPCLPCLPTLIGTPVKIGEGLMADFQS	DR	InterPro: IPR00198; RhogAP.
QY	360	RMPISIVVHCVNIEORGILTETGLYRISGCDRTVKEKEFRLVKTPVPLSKVDDHAIC	DR	InterPro: IPR00936; RhogAP.
Db	360	RMPISIVVHCVNIEORGILTETGLYRISGCDRTVKEKEFRLVKTPVPLSKVDDHAIC	DR	Pfam: PF00130; Cl_1; 1.
Db	359	PWTRSRKRTGTLQPMNSDSTNSRQLEPRTRDSDVGTPOSQGMRLHDPSVTKPES	DR	Pfam: PF00520; RhogAP; 1.
QY	420	SILKDFIRNLKPLTFLRNLRAFMEAABTDENSIAMYQAVGELPQANDTIAFLMH	DR	PRINTS; PRO053; 4FESFRDOKIN.
Db	419	GFLKDFIRNLKPLTFLRNLRAFMEAABTDENSIAMYQAVGELPQANDTIAFLMH	DR	SMART; SM00324; RhogAP; 1.
QY	480	LORVAQSPHTKMDVANLAKVFGTIVAHAVPNPDVPMQSQIKRQPVKVERLISLPLEW	DR	PROSITE; PS00470; DAG PE_BIND_DOM_1; 1.
Db	479	LORVAQSPHTKMDVANLAKVFGTIVAHAVPNPDVPMQSQIKRQPVKVERLISLPLEW	DR	PROSITE; PS0081; DAG PE_BIND_DOM_2; 1.
QY	540	SOPMMVQENIDPLHVNIEASFNSTPDKVSLGPGVTPERHQLKTPPSSLSRVR	DR	PROSITE; PS0238; RHOGAP; 1.
Db	539	SOPMMVQENIDPLHVNIEASFNSTPDKVSLGPGVTPERHQLKTPPSSLSRVR	DR	KW_HYPOTHETICAL PROTEIN; 629 AA; 7111 MW; BFI7BBA3456077A CRC64;
QY	600	SILTKNTPRGSKSKSATNLGROGNFFASPLK	DR	SBQUENCE 629 AA; 7111 MW; BFI7BBA3456077A CRC64;
Db	597	STISKNTPMGGSKSKASSI-PRQGNFFASPLK	DR	Query Match 76.4%; Score 2476.5; DB 2; Length 629;
RESULT 9				
QY	61	QKSALALI-NRGOPSSNAGNKLSTIDESGSTLSDISFDKIDESLDWSSILVKFLKK	RA	Best Local Similarity 75.5%; Pred. No. 3.6e-145; Matches 478; Conservative 77; Mismatches 73; Indels 5; Gaps 4;
Db	61	TETERSLEVULKHARNQDVDEIKRORAAECEKUERQIOLIREMLMDTSQIOLSEQ	RA	1 MDPMMLNVLNRLFOLVVERTEILESEGNTQFOILOKQDFEDFRKWORDHLCGKQDILMK 60
QY	121	QKSALALI-NRGOPSSNAGNKLSTIDESGSTLSDISFDKIDESLDWSSILVKFLKK	RA	1 MATNMMLNRLFOLMQLQDGNLNEGIEPOFIOLAKNEFDRRKWQKSEQELIKNKENLMK 60
Db	121	QKSALALI-NRGOPSSNAGNKLSTIDESGSTLSDISFDKIDESLDWSSILVKFLKK	RA	QY 61 ASTERSALDVULKHARNQDVDEIKRORAAECEKUERQIOLIREMLMDTSQIOLSEE 120
QY	180	REKRSRSRQFVDPGPVKRSIGAVDQNEVAKTIVPVDGPGPTEAVSTIETV	RA	61 TETERSLEVULKHARNQDVDEIKRORAAECEKUERQIOLIREMLMDTSQIOLSEQ 120
Db	180	REKRSRSRQFVDPGPVKRSIGAVDQNEVAKTIVPVDGPGPTEAVSTIETV	RA	QY 180 REKRSRSRQFVDPGPVKRSIGAVDQNEVAKTIVPVDGPGPTEAVSTIETV 120
QY	240	PWTRSRKRTGTLQPMNSDSTNSRQLEPRTRDSDVGTPOSQGMRLHDPSVTKPES	RA	Db 181 REKRS-SRQHTEGPVPSKRNSIGAVDQNEVAKTIVPVDGPGPTEAVSTIETV 120
Db	240	PWTRSRKRTGTLQPMNSDSTNSRQLEPRTRDSDVGTPOSQGMRLHDPSVTKPES	RA	QY 240 PWTRSRKRTGTLQPMNSDSTNSRQLEPRTRDSDVGTPOSQGMRLHDPSVTKPES 120
QY	300	CYPCGKRITKFGKLSLKRDCRVSHPCCRDPCLPCLPTLIGTPVKIGEGLMADFQS	RA	Db 300 CYPCGKRITKFGKLSLKRDCRVSHPCCRDPCLPCLPTLIGTPVKIGEGLMADFQS 120
Db	300	CYPCGKRITKFGKLSLKRDCRVSHPCCRDPCLPCLPTLIGTPVKIGEGLMADFQS	RA	QY 300 CYPCGKRITKFGKLSLKRDCRVSHPCCRDPCLPCLPTLIGTPVKIGEGLMADFQS 120
QY	360	RMPISIVVHCVNIEORGILTETGLYRISGCDRTVKEKEFRLVKTPVPLSKVDDHAIC	RA	Db 360 RMPISIVVHCVNIEORGILTETGLYRISGCDRTVKEKEFRLVKTPVPLSKVDDHAIC 120
Db	359	PWTRSRKRTGTLQPMNSDSTNSRQLEPRTRDSDVGTPOSQGMRLHDPSVTKPES	RA	QY 359 PWTRSRKRTGTLQPMNSDSTNSRQLEPRTRDSDVGTPOSQGMRLHDPSVTKPES 120
QY	420	SILKDFIRNLKPLTFLRNLRAFMEAABTDENSIAMYQAVGELPQANDTIAFLMH	RA	Db 420 SILKDFIRNLKPLTFLRNLRAFMEAABTDENSIAMYQAVGELPQANDTIAFLMH 120
Db	419	GFLKDFIRNLKPLTFLRNLRAFMEAABTDENSIAMYQAVGELPQANDTIAFLMH	RA	QY 419 GFLKDFIRNLKPLTFLRNLRAFMEAABTDENSIAMYQAVGELPQANDTIAFLMH 120
QY	480	LORVAQSPHTKMDVANLAKVFGTIVAHAVPNPDVPMQSQIKRQPVKVERLISLPLEW	RA	Db 480 LORVAQSPHTKMDVANLAKVFGTIVAHAVPNPDVPMQSQIKRQPVKVERLISLPLEW 120
Db	479	LORVAQSPHTKMDVANLAKVFGTIVAHAVPNPDVPMQSQIKRQPVKVERLISLPLEW	RA	QY 479 LORVAQSPHTKMDVANLAKVFGTIVAHAVPNPDVPMQSQIKRQPVKVERLISLPLEW 120
QY	540	SOPMMVQENIDPLHVNIEASFNSTPDKVSLGPGVTPERHQLKTPPSSLSRVR	RA	Db 540 SOPMMVQENIDPLHVNIEASFNSTPDKVSLGPGVTPERHQLKTPPSSLSRVR 120
Db	539	SOPMMVQENIDPLHVNIEASFNSTPDKVSLGPGVTPERHQLKTPPSSLSRVR	RA	QY 539 SOPMMVQENIDPLHVNIEASFNSTPDKVSLGPGVTPERHQLKTPPSSLSRVR 120
QY	600	SILTKNTPRGSKSKSATNLGROGNFFASPLK	RA	600 SILTKNTPRGSKSKSATNLGROGNFFASPLK 120

RP	SEQUENCE FROM N.A.
RC	TISSUE-Embryo;
RA	Klein S., Strausberg R.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RL	EMBL; BC046676; AAH46676.1; -.
DR	HSSP; Q98935; IFC;
DR	GO; GO:00105489; F:electron transporter activity; IEA.
DR	GO; GO:00105505; F:ion ion binding; IEA.
DR	GO; GO:0006118; P:electron transport; IEA.
DR	GO; GO:0017242; P:intracellular signaling cascade; IEA.
DR	InterPro; IPR001450; 4Fe4S ferredoxin.
DR	InterPro; IPR002219; DAG PE-bind.
DR	InterPro; IPR000198; RhoGAP.
DR	InterPro; IPR008936; Rho_GAP.
DR	PFam; PF00130; CL_1; 1.
DR	PFam; PF00620; RhoGAP; 1.
DR	PFam; PF00109; CL_1; 1.
DR	SMART; SM00324; RhogAP; 1.
DR	SMART; SM00324; RhogAP; 1.
DR	PROSITE; PS0079; DAG PE_BIND_DOM_1; 1.
DR	PROSITE; PS0081; DAG PE_BIND_DOM_2; 1.
DR	PROSITE; PS50238; RhogAP; 1.
SQ	SEQUENCE 629 AA; 70961 MW; 6DB83C592270FD4 CRC64;
	Query Match 75.9%; Score 2462.5; DB 2; Length 629; Best Local Similarity 75.2%; Pred. No. 2.6e-144; Mismatches 476; Conservative 77; Mismatches 75; Indels 5; Gaps 4;
Oy	1 MOTMMLNVLNLFOLVRVVEILSEGNEVQFQLAKDFEDRKWQRTDHELGKQDLMK 60
Db	1 MATMLMLNRLNLFOLMROVDGLNEGIEPOFIOLAKTFEARRKWQKSOEQLMKENKMLMK 60
Oy	61 AETERSALDVKUQKHARNQVDVEIKRQRAEADCEKLERQIQLTREMIMCD-TSGSIQSEE 120
Db	61 TETERSALEVKUQKHARNQVDVEIKRQRAEADCEKLERQIQLIRELUMCDPCSIQSEQ 120
Oy	121 QKSLAFLAFNTRTOMSADGNTRKLISKEDASILSDISFDKTEDSLWDSSLVNVLKK 179
Db	121 QKSLAFLAFNTRTOMSADGNTRKLISKEDASILSDISFDKTEDSLWDSSLVNVLKK 180
Oy	180 REGRSTSRSQFUDGPGVVKRKSIGSAVQDGQNEISVAKTTVVPNDGGPIERAVSTETV 239
Db	181 REKRRS-SRQHTEGGPPVPSKRSNSVQGALDQANESIATKTTVVPNDGGPIEVSTETV 239
Oy	240 PWYTRSRKRTGTMQPMNSDSTSINRSQLRPRETERDSVGTPOQNSGMRJADPFSKTVIKES 299
Db	240 PYNTRSRRTGTIOPWNNSDSSLVSRHLDKGEIDSFRTPQ-NGGMRLHEFVSKTVIKES 298
Oy	300 CVPCKGKIKFGKUQKSRDCRVCSPCRDCPCLCPTLIGPVKIGEMQMLADFSQTS 359
Db	299 CVPCKGKIKFGKUQKSRDCRVCSPCRDCPCLCPTLIGPVKIGEMQMLADFSQTS 358
Oy	360 PMPSPIVHCVNVEIQRQLETTGLYRISGCCDRTVKELEKEFLRVTPLLSKDDHAIIC 419
Db	359 PMPSPIVHCVNVEIQRQLETTGLYRISGCCDRTVKELEKEFLRVTPLLSKDDHAIIC 418
Oy	420 SLKDFLRLNKEPLTFLRNLNRAFMEAETTDENSIAAMYQAVGELPQANRDTLAFMLH 479
Db	419 GELKDFLRLNKEPLTFLRNLNRAFMEAETTDENSIAAMYQAVGELPQANRDTLAFMLH 478
Oy	480 LORVAQSPHTKMDVANLAKVAFPTIVAAVNPNDPVTMDSQDTRKQPKVVERLSPBYW 539
Db	479 LORVAQSPDCKMDVSNLARVFGPTLVLGHAVSDPDMTQDTRQPMVTERLISLSPBYW 538
Oy	540 SQFMVQDQENIDPLHVTIENSAFSTPQDPKSLGVTTPHQQLKTPSSSSLQRVR 599
Db	539 NQPMMV- ENTDPHNTIENAVNVTPTOPDGRVSLGSLBLTPEQQFKKTPSSSSLQRVR 596
Oy	1 MOTMMLNVLNLFOLVRVVEILSEGNEVQFQLAKDFEDRKWQRTDHELGKQDLMK 60
Db	1 METAVMMHHSIERSRQADVNEESTRQFQDQATNEEDNRKWRLEQELACKELTK 60
	Query Match 67.0%; Score 2173; DB 2; length 654; Best Local Similarity 64.6%; Pred. No. 2.5e-126; Mismatches 425; Conservative 104; Mismatches 99; Indels 30; Gaps 9;
Oy	61 AETERSALDVKUQKHARNQVDVEIKRQRAEADCEKLERQIQLIRELUMCD-TSGSIQSEE 119
Db	61 AETERSALEVKUQKHARNQVDVEIKRQRAEADCEKLERQIQLIRELUVSEGSSSIQSEE 120
Oy	120 EOKSALFLN-RQPSSSNAGKRLSTIDESGILSDISFDKTEDSLWDSSLVKTPFLK 178

Db	121 BQRSAAFLNRSQRNQPNLNTSRLATIDBASILSDISYKTDSDLWDSAIRVRLK 180	RN [2] SEQUENCE FROM N.A.
Qy	179 KREKRSTSROFDGPPGVKTRSTGSAVQNESTVAKTVTVNDGGIEAVSTIET 238	RP TISSUE=Whole;
Db	181 KROKRRS-SRNHTEGPPAAKRSRSTORTSKGNESLIVAKTVTVFADGGIEAVTVEA 239	RA Strausberg R.; Submittd (DEC-2003) to the EMBL/GenBank/DBJ databases.
Qy	239 VPYWTSRRK-----GTLQPNSDTINSROLE-----PRTEIDS-VG 276	RL EMBL; BC003983; AAH3983.1; -.
Db	240 VPYWTSRRKTVFCSSBQCISLNYSAAVENTDVTDSVOSMDVFKQPSLNAENRAEPS 299	DR EMBL; BC003983; AAH3983.1; -.
Qy	277 TPOSNGGMLRHDIFVSKVNIKPSBCVPGKRIKFGKLSIKCDCRVLVSHPEFRDCPLCI 336	RW Hypothetical protein.
Db	300 TPOQNGGVRHLFISKVVKIKPSBCVPGKRIKFGKLSIKCDCRVLVSHPEFRDCPLCI 359	SEQUENCE 654 AA; 73198 MW; CB656C1758B86DDB CRC64;
Qy	337 PTLIGTPVKIGBMLADFVQSPMPSIVVHCVNETEQRLGETETGILYRIGCDRTVKE 396	SO Query Match 67.0%; Score 2173; DB 2; Length 654;
Db	360 PSMTGTPVKIGBMLADFVQSPMPSIVVHCVNETEQRLGETETGILYRIGCDRTVKE 419	Best Local Similarity 64.6%; Pred. No. 2.5e-126; Matches 425; Conservative 104; Mismatches 99; Indels 30; Gaps 9;
Qy	397 KERFLRKTVPLSKVDIHAICSLIKDFLNLKPELTFILRNLRAFMEARITDENSIA 456	Db 61 AETERSALDVKKHARNOVDEIIRRQKAASSDCAKDLQIOLIREMLCD-TSGSIQLE 119
Db	420 KERFLRKTVPLSKVDIHAITGLKDFLNLKPELTFILRNLRAFMEARITDENSIA 479	121 BQSKALFLN-RGQPSNSAGKRLSTIDESGSIISDISFQDTESLDWDSSLVVKFLK 178
Qy	457 AMYQAVELPQANRDTIAFLMHLQRAQSHTKMDVANLAKVFGITVAHAVPNDDPT 516	61 AETERSALDVKKHARNOVDEIIRRQKAASSDCAKDLQIOLIREMLCD-TSGSIQLE 120
Db	480 LMTQNTISDLPQPHRDTIAFLIHLQRAQSHTKMDVANLAKVFGITVAHAVPNDDPT 539	121 BQSKALFLN-RGQPSNSAGKRLSTIDESGSIISDISFQDTESLDWDSSLVVKFLK 180
Qy	517 MSODIKQPKVVERLISLPLEWSQFMNVEGENIDPLH-VIENNSNASTPQTPDIKSSL 575	179 KREKRSTSROFDGPPGVKTRSTGSAVQNESTVAKTVTVNDGGIEAVSTIET 238
Db	540 ILQDTKQPRVERLISLPLEWSQFMNVEGENIDPLH-VIENNSNASTPQTPDIKSSL 596	181 KROKRRS-SRNHTEGPPAAKRSRSTORTSKGNESLIVAKTVTVFADGGIEAVTVEA 239
Qy	576 GVVTPPHQLKTPSSSSLSQVR-STLKTPRFSKSKATNLGRQGNFASPLIK 632	239 VPYWTSRRK-----GTLQPNSDTINSROLE-----PRTEIDS-VG 276
Db	597 GPITTPDQMSKTPSSSSLSQVR-STLKTPRFSKSKATNLGRQGNFASPLIK 654	277 TPOSNGGMLRHDIFVSKVNIKPSBCVPGKRIKFGKLSIKCDCRVLVSHPEFRDCPLCI 336
RESULT 13		
AAH63983	PRELIMINARY; PRT; 654 AA.	300 TPOQNGGVRHLFISKVVKIKPSBCVPGKRIKFGKLSIKCDCRVLVSHPEFRDCPLCI 359
ID	AAH63983	Qy 337 PTLIGTPVKIGBMLADFVQSPMPSIVVHCVNETEQRLGETETGILYRIGCDRTVKE 396
AC	AAH63983;	Db 360 PSMTGTPVKIGBMLADFVQSPMPSIVVHCVNETEQRLGETETGILYRIGCDRTVKE 419
DT	25-MAR-2004 (TREMBLrel. 27, Last sequence update)	Qy 397 KERFLRKTVPLSKVDIHAICSLIKDFLNLKPELTFILRNLRAFMEARITDENSIA 456
DT	25-MAR-2004 (TREMBLrel. 27, Last annotation update)	420 LMTQNTISDLPQPHRDTIAFLIHLQRAQSHTKMDVANLAKVFGITVAHAVPNDDPT 539
DE	Hypothetical protein racgpl.	Qy 480 LMTQNTISDLPQPHRDTIAFLIHLQRAQSHTKMDVANLAKVFGITVAHAVPNDDPT 539
GN	RacGAP1.	Db 517 MSODIKQPKVVERLISLPLEWSQFMNVEGENIDPLH-VIENNSNASTPQTPDIKSSL 575
OS	Brachydanio rerio (Zebrafish) (Danio rerio).	Db 540 ILQDTKQPRVERLISLPLEWSQFMNVEGENIDPLH-VIENNSNASTPQTPDIKSSL 596
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.	Qy 576 GVVTPPHQLKTPSSSSLSQVR-STLKTPRFSKSKATNLGRQGNFASPLIK 632
OX	NCBI_TaxID=7955;	Db 597 GPITTPDQMSKTPSSSSLSQVR-STLKTPRFSKSKATNLGRQGNFASPLIK 654
RP	SEQUENCE FROM N.A.	Qy 1 [1]
RC	TISSUE=Whole;	Db 2 [1]
	MEDLINE=22388257; PubMed=12477932; Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Seare M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullally S.J., Bosis S.A., McElvan P.J., McKernan K.J., Malek J.A., Gunnarson P.H., Richards S., Worley K.C., Haile S., Garcia A.M., Gay L.J., Huijyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shvchenko Y., Boulard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Gimmon J.J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalius D.E., Schmerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	Db 3 [1]
RT	RL	Qy 1 [1]
RESULT 14		
Qy	06DF11 PRELIMINARY; PRT; 612 AA.	Qy 1 [1]
DB	06DF11; 01-OCT-2004 (TREMBLrel. 28, Last sequence update)	AC 06DF11;
DT	01-OCT-2004 (TREMBLrel. 28, Last sequence update)	DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Hypothetical protein (Fragment)	DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)
OS	Xenopus laevis (African clawed frog)	DE Hypothetical protein (Fragment)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;	OS Xenopus laevis (African clawed frog)
OC	Xenopodinae; Xeropopus.	OC Xenopodinae; Xeropopus.
OX	NCBI_TaxID=8355;	OX NCBI_TaxID=8355;
RP	SEQUENCE FROM N.A.	RP [1]

RA	diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soarez M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Baha S.S., Lequeillano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Boak S.A., Ebdon P.J., McKernan K.J., Malek J.A., Guinaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimes J., Schnitz J., Myers R.M., Butterfield Y.S.,
RA	Krzewinski M.I., Skalska U., Smalius D.E., Schnarch A., Schein J.E.,
RA	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RT	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE-Ovary; MEDLINE-22341132; PubMed=12454917;
RX	Klein S.I., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P., submitted (JUN-2004) to the EMBL/GenBank/DBJ database.
RA	"Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.", Dev. Dyn. 225: 384-391 (2002).
RL	[3]
RN	SEQUENCE FROM N.A.
RC	TISSUE-Ovary; Klein S., Strausberg R., Wagner L., Pontius J., Clifton S.W., Richardson P., submitted (JUN-2004) to the EMBL/GenBank/DBJ database.
RA	"Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.", Dev. Dyn. 225: 384-391 (2002).
RT	[1]
RP	SEQUENCE FROM N.A.
RX	PUBMED=14702039;
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagahari K., Kimura K., Makita H., Sekine M., Ohayashi M., Nishi T., Shihabara T., Tanaka T., Isono S., Yamamoto J., Saito K., Kawai Y., Isono I., Nakamura Y., Nagahari K., Murakami J., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoi T., Kaku Y., Kodaira H., Kikkawa E., Omura Y., Takahashi M., Kanda K., Yokoi T., Furuya T., Murakami T., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Niromiya K., Ishihara T., Yamashita H., Murakami K., Fujimori K., Tani H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togita S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Muashishino K., Yuki H., Oshima A., Sasada N., Aotsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriya S., Moniyama H., Satoch N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H., Hisamatsu K., Watanabe K., Sugiyama A., Tokemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi I., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada F., Fujii T., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikeda Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta S., Senba T., Makamura K., Nakamura Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura M., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., "Complete sequencing and characterization of 21,243 full-length human cDNAs.", Nat. Genet. 36:40-45 (2004).
RA	241 TVEAVPVR-RRSRKSRAISSLQDHSTSVLPQINED---EKEMEPENVPNHPKPKP---TR 290
RA	286 LHDVFSKTVKPECPVPGKRIKKGKLSKURDRERWVSHPRCPPLCIPYL--IGP 343
RA	291 THVYLSRTMRAEVCMVCGKVKRCKMCLCKDRERLILRPECKOPCPKVCSSTFPSQSTI 350
RA	344 VKIGEGLADPFVQSOTSPMSIVPHCVNTEORGITETGYRISGCDRTVKEKKFLRV 403
RA	351 LKNGPGVLAQDAPAMPVPRPSLVLQCVNELEKGRGERGYRICDRLVKEKKFLRV 410
QY	404 KTVPLLSKQDDTHACSLIKDFLRNKLPLTRLNRFMEAETIDDSNIAWYQVG MEDLINE-22380257; PubMed=12477932;
RA	411 KTKAQHLAKEDDIHVGALKEFFRTLQPLTISLHATPLDAADILDCGDRABTCQHV
RA	464 BLPOAQRDTLAFMLMHQVRQASPHKMDVANLAKVFGPTIVAHAVPPDPVTMSQDKR
RA	471 DLPAQPNRDTLAFMLHLYPRMVSSECKNDTNAIARIGPTLVGYSAPNPSPLQMOPDR
RA	524 OPKVVERLISLPLPEWSQFMMEVGECNIDPLHVIENSNAPSTPQTDPDIKVSLLGVTTPH
RA	531 QAKOMSLLISIPIGRFWNQFLFTNOENKOSAKLQE-----RLFPLTSPE-
Db	584 QLUKTPSSSLSLSQDVRVSTLTKNPFRFGSKSASATNLGQGNFRASP 629
Db	576 -INSASS-----LLKTPCLAQSASKSDLPLKIGAGRFTSP 610
QY	RESULT 15
RA	Q9H9L9 ID Q9H9L9 PRELIMINARY; PRT; 255 AA.
RA	DT Q9H9L9; 01-MAR-2001 (TREMBL 16, Created)
DT	01-MAR-2001 (TREMBL 16, Last sequence update)
DT	01-MAR-2004 (TREMBL 26, Last annotation update)
DE	Hypothetical protein FLW12664.
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	PUBMED=14702039;
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagahari K., Kimura K., Makita H., Sekine M., Ohayashi M., Nishi T., Shihabara T., Tanaka T., Isono S., Yamamoto J., Saito K., Kawai Y., Isono I., Nakamura Y., Nagahari K., Murakami J., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoi T., Kaku Y., Kodaira H., Kikkawa E., Omura Y., Takahashi M., Kanda K., Yokoi T., Furuya T., Murakami T., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Niromiya K., Ishihara T., Yamashita H., Murakami K., Fujimori K., Tani H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togita S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Muashishino K., Yuki H., Oshima A., Sasada N., Aotsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriya S., Moniyama H., Satoch N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H., Hisamatsu K., Watanabe K., Sugiyama A., Tokemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi I., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada F., Fujii T., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikeda Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta S., Senba T., Makamura K., Nakamura Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura M., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., "Complete sequencing and characterization of 21,243 full-length human cDNAs.", Nat. Genet. 36:40-45 (2004).
RA	DR EMBL; AK022726; BAB14206.1; -.
DR	InterPro; IPR000198; RHOGAP
DR	InterPro; IPR008936; RHOGAP
DR	HSSP; Q8935; 1FC
DR	SMART; SM0034; RHOGAP
DR	PROSITE; PS50238; RHOGAP
DR	SEQUENCE 255 AA; B59D7B59385821BD CRC64;
DR	B59D7B59385821BD CRC64;

Best Local Similarity 99.2%; Pred. No. 2e-65; Matches 234; Conservatory 0; Mismatches 2; Indels 0; Gaps 0;

QY 397 KEEFLRIVKTVPLISKVUDTHAICCSLLKDFPLRNLKEPLTFRNRAFMEEAETDENSIA 456

Db 20 KIKFLRIVKTVPLISKVUDTHAICCSLLKDFPLRNLKEPLTFRNRAFMEEAETDENSIA 79

QY 457 AMYQAVGELPQANRDTLAFMLTHLQRVAQSPHTKMDVANLAKVFGPTIVAAVPNPDPVT 516

Db 80 AMYQAVGELPQANRDTLAFMLTHLQRVAQSPHTKMDVANLAKVFGPTIVAAVPNPDPVT 139

QY 517 MSQDIKQPKVVERLISPLIETWSQFMVQEIQENIDPLHVIENSAESTPQDPIKSLG 576

Db 140 MLQDIKQPKVVERLISPLIETWSQFMVQEIQENIDPLHVIENSAESTPQDPIKSLG 199

QY 577 PVTTPHQQLKTPSSSLISQRVSTLTKNTPRPGSKSKSATNLGROONFFASPMLK 632

Db 200 PVTTPHQQLKTPSSSLISQRVSTLTKNTPRPGSKSKSATNLGROONFFASPMLK 255

Search completed: February 1, 2005, 14:19:02
 Job time : 208 secs